Visage 7 Client

User Manual

VISAGE IMAGING®
Visioneering Science for Life

CE 1275

This software is CE-compliant and is defined as a class IIa medical device in accordance with Medical Devices Directive 93/42/EEC.

All product and company names are trademarks or registered trademarks of the respective companies.

Some of the specifications described herein may not be currently available in all countries. Please contact your local sales representative for the most current information.

> Caution:
> US federal law restricts this device to sale by or on the order of a physician (or properly licensed practitioner).

Visage 7 is the successor of the Visage PACS/CS product family.

Information in this manual may be subject to changes without prior announcement.

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System Overview

In this section you will find an overview of the Visage® 7 product and its data security concept, as well as a brief introduction to the Visage user documentation.

Intended use

Visage is a system for distributing, viewing, processing, and archiving medical images within and outside health care environments.

The Visage server receives image data in DICOM format via the hospital network. This provides universal connections to archives, modalities, and workstations. The supported modalities are listed in the DICOM Conformance Statement.

Besides general image interpretation and processing tools, Visage provides specific tool sets for several clinical applications, including:

- CT/MR angiography, e.g. for vascular analysis and stent planning
- Cardiac analysis, including calcium scoring and functional assessment of cardiac CT data
- Neuroradiology, including CT and MR brain perfusion analysis
- Oncology, including SUV analysis and lesion marking and analysis

Visage is to be used only by trained and instructed health care professionals. It can support physicians and/or their medical staff in providing their own diagnosis for medical cases. The final decision regarding diagnoses, however, resides with the doctors and/or their medical staff in their own area of responsibility.

Although the web and thin client technologies allow the software to be run on a variety of hardware platforms, for diagnostic purposes the user must make sure that the display hardware used for reading the images complies with state-of-the-art diagnostic requirements and currently valid laws.

Only DICOM for presentation images can be used on an FDA approved monitor for mammography for primary image diagnosis.

Only uncompressed or non-lossy compressed images must be used for primary image diagnosis in mammography.

License management

Every Visage installation comes with a license code. Without it the software will not run on the server.

Licenses

The license code serves as copy protection and controls which product options are enabled. This includes:

- The maximum number of DICOM connections for calling/importing data from the network onto the Visage system, and for sending data from the Visage system.

- How many users may access data on the server simultaneously via Visage Web Client, or via Visage 7 Client (also referred to as thin client). Different viewer types require different licenses.

- The maximum data volume on the server.

- Activation/deactivation of audit trails.

- The availability of the archive option.

- The availability of the cardiac analysis option for Visage 7 Client.

- The availability of the oncology option for Visage 7 Client.

- The availability of the neuro option for Visage 7 Client.

Visage uses the so-called "floating licenses" concept. This means that a license is not bound to a particular user name or a dedicated workstation or computer. A license for 10 users means that 10 users can work with Visage 7 Client simultaneously. If an 11th user tries to log on, he or she is told to try again later. Once one of the original 10 users logs off, logon of the 11th user will be permitted. Of course, licenses can be upgraded.

Upgrade

When upgrading an installation, the old license becomes invalid. The new Visage license, which comes with the upgrade, must be installed.

If a larger data volume was licensed in a previous version, this may lead to the oldest data being deleted from the system after the new license has been installed, depending on the "auto-delete" settings defined by the system administrator.

System requirements

When describing system requirements we make a distinction between server and clients.

Server

Visage runs on standard server platforms. Server hardware must be qualified by Visage Imaging. For a detailed server hardware and software specification please contact your sales representative.

Clients

These are the minimum hardware and software requirements for Visage 7 Client PCs or Macs.

- **Operating system and software**

  Microsoft Windows XP (32 bit and 64 bit editions),

  Microsoft Windows Vista (32 bit and 64 bit editions),

  Microsoft Windows 7 (32 bit and 64 bit editions),

  Mac OS X 10.5, or

  Mac OS X 10.6.

- **Computer/processor**

  Intel Pentium IV or equivalent

- **Main memory**

  1 GB RAM

- **Graphics card**

  Any graphics card that supports a screen resolution of at least 1024 x 768 pixels and true color.

  For optimum performance on very high resolution monitors, we recommend graphics cards supporting *OpenGL* acceleration. For details on qualified cards please contact your Visage Imaging representative.

- **Monitor**

  Single monitor or up to four monitors for viewing and one or more additional monitors for study browser, reporting, or quality assurance. All monitors used for viewing image data must have the same pixel resolution and orientation (portrait or landscape).

- **Other**

  For latency free operation in local area networks (LAN) we recommend the use of Gigabit Ethernet.

  In order to be able to use the client in wide area networks or through the Internet, the Visage streaming technology has been optimized to support even very slow networks, down to a bandwidth of 512 Kbit/s. However, for smooth operation we recommend a bandwidth of more than 6 MBit/s and a latency of less than 60ms.

Temporary harddisk space: If you intend to create movies on the **Cine** tool card of the Visage 7 Client the system will temporarily occupy local harddisk space during movie creation (min. 1 GB or more for large movie files).

Data protection and data security

Data relating to individuals is subject to data protection. In this regard, please ensure compliance with all applicable laws and regulations in your country.

Visage provides extensive security mechanisms that help you assure data protection and data security.

On the administration platform the system administrator can also activate the audit trail option. This supports the strict regulations concerning patient data protection and data security according to US law.

Note
For security reasons, it is not permitted to make changes to the Visage product and its database. Contravention of this will lead to all guarantees being revoked and under some circumstances may even be violating applicable laws.

Access control and authentication

Each user must log into the Visage system with a **user name** and **password**. The Visage server checks these entries. Only if they match is access to the system granted. Access authorization ensures that users can only view data for which they have access rights.

Login and password To ensure that user accounts and their passwords are effectively protected from unauthorized access:

- passwords are encrypted

and, if this has been configured

- passwords will expire
- failed login attempts are recorded, and multiple failed login attempts will cause a user account to be locked.

Note
Recording logins and other actions only makes sense if all users on the system have their own user names and passwords.

Multi-session operation

A user may log on to Visage more than once from a single or multiple client machines. This allows users to work from more than one clinical workplace simultaneously and view the same data there.

Each session makes use of (and thereby blocks) one license.

Auto logoff

Visage can be configured so that a logged in user is logged off from the system after a configurable period of time with no user interactions. This prevents licenses from being unnecessarily blocked and stops any unauthorized persons accessing data if a user has logged on but has forgotten to log off again.

Service access permissions

Remote access for service purposes must be granted explicitly. It is therefore up to you if and to what extent you wish to grant access rights to service.

- Full Access

  Service has read and write permissions. This means that service personnel can analyze problems and can solve these problems or change settings. Service access is logged.

- Limited Access

  Service has read permission only.

- No Access

  Service has no access.

Note

Please note that with full access, service is granted unlimited access. Under certain circumstances this may include patient data which has not been anonymized.

Audit trails

Logging of user actions in Visage 7 Client occurs in so-called audit trails. Audit trails are recordings of access-controlled actions. They are the proof that access to patient data is monitored.

A message informs users that their actions may be monitored.

The following activities are recorded if the audit trail option has been activated by the system administrator:

- Changes to access rights with accessing user, date and time

- Viewing, exporting, printing, or deleting patient data

- Changes to archived images with time, date and user

- Login and logout, and failed attempts to log in

- Every query/retrieval

- Service sessions (local or remote)

- Software updates, as well as backup and restore

In addition the highest original number of images is recorded, to compare with the current number of images.

If audit trails must be kept for a number of years, it is the responsibility of the system administrator to ensure that the relevant log files are archived according to the requirements that apply to your institution and country.

The system administrator is the only user who has access to the audit trails via a dedicated viewer.

For larger systems, a separate database server can be made available for audit trails.

Overview of the product documentation

The Visage product documentation distinguishes between three user groups and the tasks that these groups typically perform.

- Clinical users

    These users access the Visage server from a Visage Web Client or Visage 7 Client in order to review 2D, 3D, or report data.

    The Visage Web Client and Visage 7 Client **user documentation** addresses this user group.

- System administrator

    The system administrator of the hospital will perform system maintenance and adapt server configuration and database settings to changes in the system and network environment. This user group works on the administration platform.

    The Visage **administrator documentation** addresses this user group.

- Service personnel

    This user group will install the system and subsequently perform initial system configuration. This group will need the **installation manual** for system installation and the administration documentation for initial system configuration.

In this section you will find an overview of the available product documentation as well as information on how to work with the Visage manuals and online help systems.

User and administrator documentation

The Visage product documentation addresses the information needs of each of these user groups.

User documentation   The Visage Web Client and Visage 7 Client user documentation addresses clinical users.

It comprises:

- The **Visage Web Client** user documentation

  In these documents clinical users will find a complete description of the Visage Web Client user interface and program functionality.

  In the printed **user manual** you will find a complete description of all Visage Web Client functions.

  The **online guide** offers additional information and task-oriented descriptions presented in a step-by-step style. Online guides are available in English and German.

  Visage Web Client also features a **context-sensitive online help system** which you can call up right from the user interface. The context-sensitive help topics explain all the user interface elements and features of the currently displayed window in your native language. For the English and German user interface the online help system also contains task-oriented step-by-step instructions.

- The **Visage 7 Client** user documentation

  The **user manual** (this document) provides a complete description of all Visage 7 Client functions.

  Visage 7 Client also features an **online help system**, which you can call up from the Help menu. The various help topics explain the user interface of the client software.

Administrator documentation   The Visage administrator documentation supports system administrators in a hospital. It helps them with user management and adapting the system to changes in the overall network environment, if this becomes necessary.

The Visage administrator documentation also helps service personnel with initial system configuration tasks immediately after system installation or update.

- The **Administration Manual**

  This document is available as a pdf file on your program CD/DVD. You can print out this document if you prefer reading on paper.

- The administration platform **Online Help System**

  The Visage administration platform features a context-sensitive online help system. The context-sensitive help topics explain the parameters you will find and the settings you can make on the various configuration windows. Whenever relevant, background information on selected topics is also given in the online help system.

Service documentation

Installation instructions are available for Visage Imaging service personnel only.

Release notes

Release notes contain additional useful information about the software. They focus on technical details.

Information on using the Visage manuals

Document structure

In order to help you locate relevant information in the Visage manuals quickly, they are subdivided into chapters.

In the **Visage 7 Client user manual** each chapter addresses a specific window or tab card of the Visage 7 Client application program. The chapter on starting and ending the program and the *Getting Started* chapter address new users of the system specifically.

The *Table of Contents* and *Index* sections help you locate a topic quickly.

Layout conventions

To help you find and interpret the appropriate information, the following visual orientation aids are used here:

• Operating steps

Single-step actions are presented as plain text.

1. Operating steps in sequences of actions are numbered.

• **Bold** text

Names of windows, menus, and functions are shown in bold typeface. Sections of text given particular emphasis are also highlighted in bold type.

Tips, notes, warnings

Tips, notes, and warnings are specifically highlighted in the text.

Tip

Tips provide additional useful information about a topic. Tips, for example, help you organize your work more efficiently.

Note

Notes mark text that you should pay special attention to. A note may, for example, emphasize a piece of information relating to the safety of functions, but where no danger is involved.
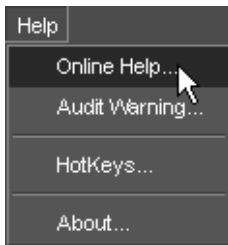

Caution

Caution is used to indicate the presence of a hazard which can cause personal injury to a patient or damage to the equipment.

Information on using the online help systems

The Visage Web Client and Visage 7 Client user interfaces, and the Visage administration platform feature an online help system each.

Calling up online help

Call up the Visage 7 Client online help window from the **Help** menu.

The first topic of the Visage 7 Client online help system is displayed.

Mac users

The Visage Client will launch the PDF viewer of your system in order to view the online documentation. Search and navigation functions depend on the PDF reader that you are using on your system. The remainder of this section does not apply.

Windows users

Use the various navigational features of the online help system to search for the information you need.

Tab cards

The left half of the Visage 7 Client online help window shows four tab cards for quick access to the help contents.
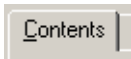
This tab card contains a table of contents similar to that of a printed book.

1. Double-click the book icon to display a topic and show subheadings.

2. Click the page with question mark icon to display the text of a help page in the right half of the help window.
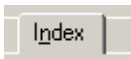
You can search for index entries here.

1. Enter a word to search for.

   -Or-

   Scroll through the alphabetical index.

2. Double-click an index entry to display the information about it.
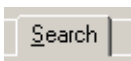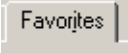
This tab card permits a full-text search.

1. Enter a word to search for.

2. Press the **RETURN** key.

   All help topics containing this word will be listed.

Favorites

On this tab card you can set bookmarks for help topics that are of particular interest to you.

1. Display the topic you want to add to the **Favorites** list.

2. Click **Add**.

Links to other topics

In various help topics you will find links that will take you to more detailed information about a subject.

Text links are highlighted by blue text color and underline.

Browse sequence

Use the **next** and **previous** icons in the footer of each help topic to scroll through the online help system topic by topic.

Help window toolbar

The upper part of the help window shows a number of icon buttons. Use these buttons to adapt the help window, scroll through topics, and print topics.

Show

Shows the online help tab cards if they are hidden and then changes to the **Hide** button.

Hide

Hides the online help tab cards if they are shown and then changes to the **Show** button.

Back

Returns to the previous topic.

Forward

Returns to the next topic (after you have clicked **Back**).

Print

Prints the current topic on the default printer.

Options

Shows a menu with more help functions.

Starting and Ending the Program

This section tells you how to start Visage 7 Client, how to log onto the server, and how to close Visage 7 Client properly.

Installing the Visage 7 Client

Before you can start Visage 7 Client for the first time you must connect your client PC or Mac to the Visage server and install the Visage 7 Client software on your computer.

1. Open your Internet browser.

2. Enter the Visage server address and "/download" in the **Address Bar**.

The Visage 7 Client download screen opens.

Windows users   Click the download link for the Visage Client .exe (Windows) under **Download Thin Client Software**.

This will start the Visage 7 Client setup procedure, which will install the client software on your PC. Follow the instructions in the setup windows.

After program installation, Visage 7 Client will be available in the Windows Start menu, and an icon will have been created on your Windows Desktop.

Mac users   Click the download link for the Visage Client .dmg (Mac) under **Download Thin Client Software**.

The .dmg file is automatically unpacked and becomes an application file (.app). You can now double-click the file to open the Visage client.

1. Copy or move the file into your **Applications** folder to install it permanently.

2. Drag&Drop the application file into the dock to create a shortcut.

Tip

From the Visage 7 Client download screen, you can also download the user manuals for the Visage 7 Client and Visage Web Client as pdf files.

Starting Visage 7 Client

If your system and user account have been configured for so-called IWA (Integrated Windows Authentication) starting the Visage 7 Client software is very straightforward.

Double-click the **Visage 7 Client** icon on your desktop.

-Or-

Select **Programs > Visage 7 > Visage 7 Client** from the Windows Start menu.

The Visage 7 Client application program opens and the **Study Browser** is shown in the foreground.

Starting Visage 7 Client from the login dialog box

If your system and user account have not been configured for IWA (Integrated Windows Authentication) or if you want to switch over to a different user interface language you start the Visage 7 Client from the login dialog box.

Windows users

Select **Programs > Visage 7 > Login Dialog** from the Windows Start menu.

-Or-
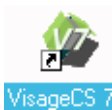
Double-click the **Visage 7 Client** icon on your desktop.

The **Visage 7 Client** login dialog box opens.
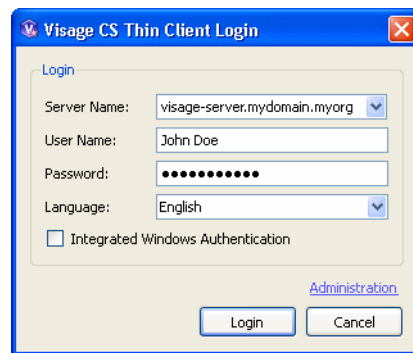
Mac users

For easy access, you should move the Visage client application to your dock

Click the **Visage 7 Client** icon in your dock.

-Or-

Double-click the **Visage 7 Client** icon in your Applications via the Finder.

All users

1. Enter the name of the server in the **Server Name** field or choose one from the list.

2. Enter your **User Name** and **Password**.

3. Select the user interface **Language**.

4. Activate or deactivate **Integrated Windows Authentication** for future program starts (not applicable for Mac users).

Note

Integrated Windows Authentication is only possible for users whose accounts were imported in the Visage system from Windows and for whom the integrated Windows authentication privilege has been set by the system administrator.

5. Click **Login** to start the program.

The Visage 7 Client application program opens and the **Study Browser** is shown in the foreground.

You can now define and start a query for case data in your database, browse through a history of recent queries and start one of those queries, or load a recent session from the session management box.

Changing your password

You should change your password from time to time for data security reasons.

1. Open the Visage 7 Client.

2. Select **File > Preferences > Change Password** from the main menu.

3. Enter your **Old Password**, the **New Password**, and repeat the new password in the **Retype New** box.

4. Press **RETURN**.

Use the new password from now on when logging in.

Exiting Visage 7 Client

Logging off from the server

In order to close **Visage 7 Client**:

Select **File > Exit** from the **Visage 7 Client** menu bar.

-Or-

 Click **Close window** in the upper right-hand corner of the window.

Mac users

In order to close **Visage 7 Client**:

Select **VisageCS > Quit VisageCS** from the **Visage 7 Client** menu bar.

-Or-

 Click the red close button in the upper left corner of the application window.

Automatic logoff   If Visage observes no activity for a certain time (default setting: 15 minutes) a message box appears. You are prompted to confirm that you wish to continue working. If you do not answer you will be logged off automatically after a few seconds. The license you were using is now available for another user.

Only the system administrator can change the automatic logout time.

Note
If you do not continue working, your current work is saved in a auto-logoff session when you are logged off automatically.

Getting Started

This section describes typical features of the Visage 7 Client:

- *The Visage 7 Client workflow*
- *The general Visage 7 Client window layout*

Note
In this user manual we assume that you have worked with Windows or Mac application programs before. You should be familiar with typical operating elements such as drop-down and context menus and various data input and selection options. You should also have experience with overall keyboard and mouse operation.

The Visage 7 Client workflow

The basic workflow with Visage 7 Client is very straightforward and indicated by the arrangement of windows on the user interface. You open these windows by selecting the respective entries in the **Window** menu or by clicking the following buttons in the upper right-hand section of the application window (Windows only).
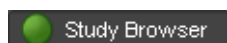
- **Study Browser**

  In the **Study Browser** you query the Visage database or connected network nodes for patient and study data. Once you have found the data you are looking for you load this data onto the **View** window. The **View** window is shown as soon as you have loaded data.

  If your Visage is integrated in another clinical software application, you may skip this step and window. In this case you select the data you wish to review in that program and then advance directly to the **View** window.

- **View**

  On the **View** window you review and analyze 3D volume datasets. You can manipulate image display and create new slice images from any position and in any orientation in the process. Moreover, you can evaluate areas of particular interest and perform various measurements and calculations. In order to document your findings you create snapshots of relevant images.

• **Export**

You use the **Export** window to create reports, which include selected snapshots and report text. Or you use the **Export** window to save snapshot images in the Visage database, to send them over the network, or to export them onto your local computer.
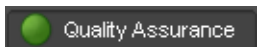
• **Quality Assurance**

You use the **Quality Assurance** window to correct or re-assign patient, study and series data manually and to match studies with orders sent by a RIS system.

The general Visage 7 Client window layout

Visage 7 Client features an intuitive user interface, which is easy to learn and allows you to perform image manipulations with a minimum of clicks. The Visage 7 Client window comprises the following basic window areas.

Menu bar	Visage 7 Client windows
Workspace of the Visage 7 Client windows	
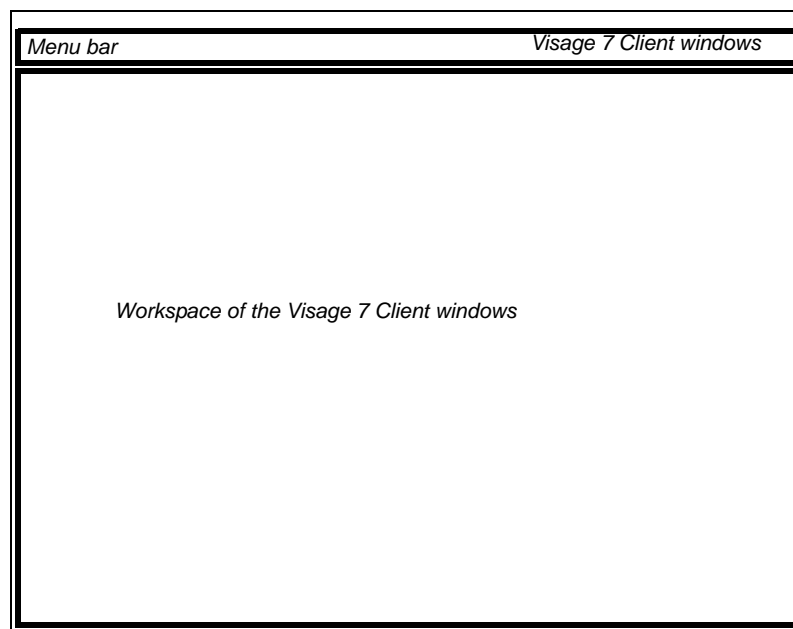
Visage 7 Client windows

The Visage 7 Client comprises four windows. You move from one window to the next by selecting the respective entries in the **Window** menu or by clicking the corresponding button (Windows only).

Note

Switching between windows does **not** load data. The new window shows the data that you queried for or loaded the last time you worked on this window.

Workspace of the Visage 7 Client windows

For a detailed description of the operating elements of the four program windows please refer to these sections:

- *Study Browser*
- *View Window*
- *Export Window*
- *Quality Assurance*

Note

If Visage 7 Client was called from another application, the **Study Browser** may not be available.

Menu bar

The Visage 7 Client main menu bar contains a number of drop-down menus for selection of program options or functions.

Context sensitivity   The Visage 7 Client program features a context-sensitive main menu. Context-sensitivity means that the contents of the menu bar depend on the Visage 7 Client window that is currently shown in the foreground. For example the **Protocol**, and **Tools** menus are available on the **View** window but not on the **Study Browser** and **Export** window.

Common commands for Windows users   These menus and commands are available on all Visage 7 Client windows.

File

Exit: Closes the Visage 7 Client.

Help

Online Help: Shows the Visage 7 Client online help system.

Audit Warning: Displays a dialog box which informs users that their activities may be monitored. This command is shown only if the audit trail license has been installed on the server.

Keyboard shortcuts: Shows the list of keyboard shortcuts for Visage 7 Client.

About: Opens a message box with information about the currently installed program version, the accessed servers, and information about the current program session.

Common commands for Mac OS users   These menus and commands are available on all Visage 7 Client windows.

VisageCS

About VisageCS: Opens a message box with information about the currently installed program version, the accessed servers, and information about the current program session.

Quit VisageCS: Closes the Visage 7 Client.
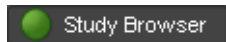
Help

Online Help: Shows the Visage 7 Client online help system.

Audit Warning: Displays a dialog box which informs users that their activities may be monitored. This command is shown only if the audit trail license has been installed on the server.

Keyboard shortcuts: Shows the list of keyboard shortcuts for Visage 7 Client.

Study Browser

The **Study Browser** is used to search for data on the local Visage server selected when logging in or partner systems (bold tabs), on a connected DICOM network node (tabs in regular typeface), or on external drives.

Basic workflow

When searching and loading data, you proceed in this order:

Local backend server or partner system

1. Query the local backend server or partner system.

2. Select one or more study or series.

3. Load this data onto the **View** window.

   -Or-

   Click **Add to View** to add the data to an ongoing Visage 7 Client session.
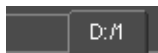
-Or-

Remote DICOM node

1. Query a remote DICOM node.

2. Select and transfer the data to the Visage database (**Retrieve** button).

3. Query the local database, for example, by insertion date today (local database tab).

4. Select the retrieved data from the local database tab card and load it onto the **View** window.

-Or-

External drive

1. Select the tab card of an external drive or directory.

2. Select the data on this tab card and load it onto the **View** window.

   -Or-

   Click **Add to View** to add the data to an ongoing Visage 7 Client session.

If this tab card is not shown in your **Study Browser**, or if it does not show the data you are looking for:

1. Select **File > Import DICOM Directory** or **File > Import DICOM Files** from the main menu.

2. Select the drive and directory where the data is stored in the **Import DICOM** dialog box and click **Choose** or **Open**.

3. Select the data on the tab card of the external drive or directory and load it onto the **View** window or select **Add to View** to add the data to an ongoing session.

Overview of the user interface
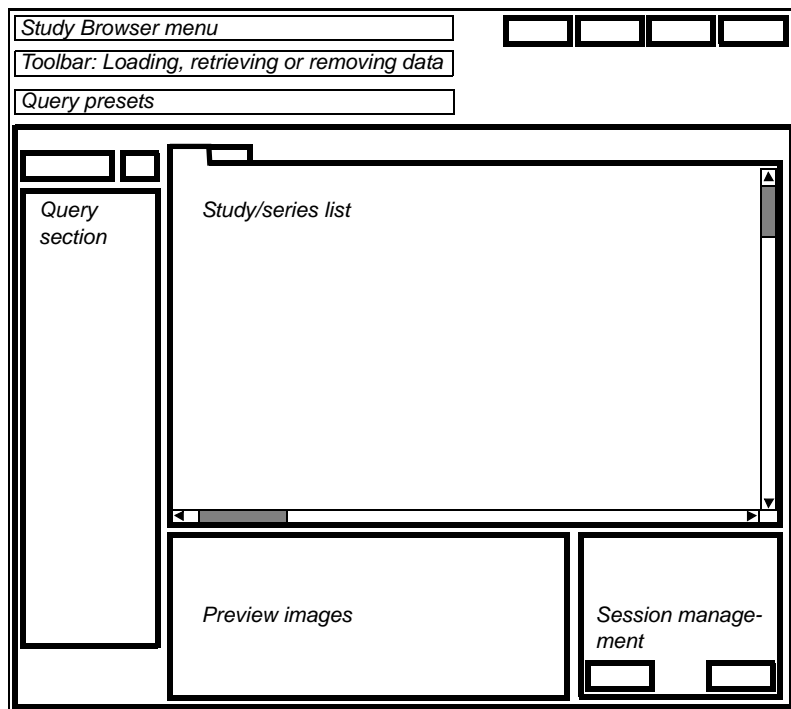
Query section

Before you start defining filter or search criteria for a database query, select the database, drive or directory you wish to search by clicking the corresponding tab above the study/series list. Any query will only apply to the database whose tab card is currently shown in the foreground.

Modality search   The query section allows you to search a database for studies performed on one or several modalities. E.g. check CT, MR, and DX modalities in the query section to show all studies and series that were performed either at the CT, **or** the MR, **or** the DX modality.

Filter criteria   All other entry boxes in the query section are filter criteria. This means, the more criteria you define, the shorter the hit list will be. E.g. enter A for patient name to show all patients whose name starts with an A. Or enter A for patient name and select today for study date to show only those patients whose name starts with an A **and** who were examined today.

Wildcard search   If you do not remember a name or number you are looking for, you can use wildcards in your search. E.g. type **Mil** in the patient name box to find **Mil**ler, **Mil**ford, **Mil**tner, or ***mil** to find all the above and also Ha**mil**ton, or **AB??34** in the patient ID box to find **AB1234**, **AB0034**, and **AB11345678**.

Even if you use wildcards, you should always specify your search criteria as precisely as possible. Rather general queries may yield a very long hit list, which would require extensive scrolling.

Filter and search criteria

Patient Allows you to search for a patient's name and ID.

Date Allows you to search for patient and study data based on a date or date range. You can toggle the date search on and off by means of the checkbox.

If toggled on, you can select or enter:

Type - select whether you want to search by **Study Date**, **Date of Birth** or **Insertion Date** (i.e. the date when the data was transferred to the server).

From *date* **To** *date* - specifies the search period. Click in a date box with the cursor and enter a date in the format YYYY-MMM-DD (e.g. 2006-MAY-23). Or click the icon button to the right of the date entry box to open a calendar and select a start and end date from here.

3. Click one of these buttons to select a default search period:

Today - selects the current day as search period.

Yesterday - selects the previous day as search period.

1 Week - selects the last seven days as search period.

2 Weeks - selects the last 14 days as search period.

Modality Allows you to search for patient and study data by modality. You can toggle the modality search on and off by means of the checkbox.

If toggled on, you can choose one of the following options:

1. Check the boxes of all those modalities whose studies you are looking for (**CT** - computed tomography, **MR** - magnetic resonance tomography, **PT** - positron emission tomography (PET), **US** - ultrasound, **CR** - computed radiography, **DX** - digital radiography, **MG** - mammography, **XA** - X-ray angiography)

2. Enter any modality abbreviations in the **Others** box (e.g. "CT"). Multiple modalities are separated by a space (e.g. "CT PT MR").

Fields Here you can specify further filter criteria.

Drop down a list of available criteria with the arrow icon to the right of a field box. Then specify your search string in the input box below the selected criterion.

For queries of your local database you can combine up to three additional filter criteria this way. For queries on DICOM nodes only two additional filter criteria can be defined: *Accession Number* and *Study Description*.

In addition, you can click **Study States...** and then select one or several study states in the dialog to be included in your search. Clicking the **Clear** button resets this selection to include all study states.

Entering a text in the **Label** box will search for labels assigned to a study by means of the *Context menu of the study/series list*. You can search for more than one label and fine-tune your search by a preceding **+** sign (label must exist) or **-** sign (this label excluded)

Starting and resetting a search
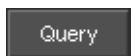
Query	Click this button to start your query of the local database or the DICOM node whose tab card is currently shown in the study/series list area.
	Click this button to remove all search criteria from the query boxes, then start defining a new search.

Query presets

The Presets bar contains the button **New Preset**, which opens a dialog to define the current settings, for example a specific query, as a preset for the currently active user. This preset will then be shown as a button on the Presets bar.
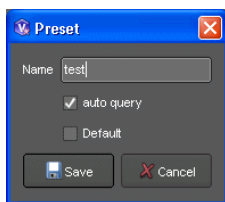
You can

- enter a name for the preset.

- check **Auto Query** to automatically start a query when the preset button is clicked.

- check **Default** to make this preset the user's default when initially opening the Study Browser window.

Context menu of the preset buttons

Clicking a preset button with the right mouse button opens this context menu.

Properties	Allows you to change the preset's name and to have the preset perform an **Auto Query** or set it as **Default**.
Default	Checking this menu option defines this preset as default, loading its parameters when the Quality Assurance view is opened.
Update Preset with Current Settings	Updates the preset with the settings currently active in Quality Assurance.
Delete Preset	Deletes the preset button after a query is confirmed.

Study/series list

The study/series list has tab cards for the local backend server of the Visage system and for each connected DICOM network node or external medium.

This Server

Click a tab to show the study/series list of the corresponding database or medium.

After switching over to another tab card, the study/series list of the last database query you performed on this tab card is shown.

Information in the study/series list

The study/series list is arranged in a hierarchical tree view. Use the **+/-** icons in front of the entries to expand or collapse this list.

For a better overview, you can sort the list by clicking on a column header. Clicking a second time reverses the search order.

Hovering with the mouse above a list entry without clicking shows information about this study in a tooltip. For example, hovering above the first column shows the assigned labels.

Patient	Name of the patient.
Patient ID	Patient's identification number.
Accession Number	Job number of the patient in the HIS/RIS (hospital or radiology information system).
Modality	Modality or modalities used to examine the patient.

Images	Number of images in a series (on study level, no image number is shown).
3D	Shows a graphical icon when a series is a 3D series (i.e. contains at least one continuous 3D volume).
	🟢 A green bullet indicates that a 3D volume dataset is available on the Visage server (local database).
	🟡 A yellow bullet indicates that the system is currently creating a 3D volume dataset from the original slice images.
Study/Series Description	Study or series description.
Study/Series Date	Date and time when the study or series was performed in the format YYYY-MMM-DD and HH:MM:SS (24 hour clock).
Insertion Date	Date and time when the study or series was sent to the local database in the format YYYY-MMM-DD and HH:MM:SS (24 hour clock).

Context menu of the study/series list

View	Loads one or more selected studies or series to the View window.
Add to View	Adds one or more selected studies or series to the View window. If this would result in data from different patients being shown on the View window, a safety query will be displayed.
View All Series Side By Side	Loads the selected series with a dynamic protocol and shows all series side by side. See also *Viewer segments* in section *View window main menu.*
View All Phases Side By Side	Loads the selected series with a dynamic protocol and shows all phases of time series side by side. See also *Viewer segments* in section *View window main menu.*
Find all Studies for this Patient	Shows all studies of the patient of the selected study.
Assign study to groups	Assigns the selected study to one or more user groups, thus granting only them access to the study. The assignment can be revoked by the same means.
Assign study to users	Assigns the selected study to one or more users, thus granting only them access to the study. The assignment can be revoked by the same means.

Study Labels...	Opens a dialog to show labels of a study and create new or assign existing labels to studies so they can be quickly located, for example for conferences or a second opinion.

1. Select a patient or study and right-click it.

2. Select **Study Labels...**

3. In the dialog now opened, check one or more existing labels in the list box (you can filter this list by means of **show public** and/or **show private**)

- OR-

Create a new label by entering a name activating **Create Private** or **Create Public** to assign it to your own account or all users.

The selected label(s) or new label will be shown in a list. You can select an entry in this list and use the context menu to perform the following actions:

- make a private label public or vice versa

- delete a label

- assign it to a button on the View window. See also *Labels tools*.

Delete protection	Protects studies from being deleted from the local database after a certain amount of time or when the database runs full and old studies would automatically be moved to remote. Also protects studies from being deleted manually during Quality Assurance activities. You can remove the delete protection later.
DICOM Send...	Sends one or more selected studies to network nodes. A dialog to select these nodes is opened.

On the **DICOM Send** tab, you can perform the following actions:

- define these nodes as default addresses for DICOM Send via **Make Default**

- apply you selection to DICOM Quick Send via **Copy to Quick Send**

On the **DICOM Quick Send** tab, you can perform the following actions:

- copy the presets to **DICOM Send**

- define these nodes as default addresses for DICOM Quick Send via **Make Default (Quick Send)**.

DICOM Quick Send	Sends one or more selected studies to one or more preselected network nodes. No confirmation is shown.
Media Export...	Sends one or more selected studies to a destination to be selected.

You can perform the following actions:

- check whether you have selected the correct **Patient**

- view the **Actual data size** of the export file(s)

- select a **Destination** in the list box

- browse for an **Export Folder**

- enter a name to the **Media Folder** or accept the the one suggested by the system

- specify the **Media Size**, selecting either **CD** or **other medium**

- specify whether to **Include Media Viewer** to view the data on the CD without additional software, **Autorun MediaViewer** when the medium is inserted and **Uncompressed only** to save in that way

Click on **Make Default** to save your settings for subsequent media exports, if required, and click on **Export** to start the export process.

Loading, retrieving or removing data

This icon is active on the local database tab and on remote DICOM nodes or external drive and for data that has already been transferred to the database.

Select one or several studies or series in the study/series list and click the **View** button.

-Or-

If you want to load only one study or series, simply double-click it in the study/series list to load the data onto the **View** window.

When session management has been enabled for your user account, double-clicking a study loads the most recent session associated with this study. Double-clicking a series loads image data only but no session information.
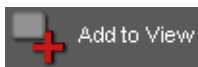
If you have already loaded data onto the **View** window and want to add more datasets rather than replace the currently loaded data:

Select the dataset you want to add to your current session on the local database tab card or the tab card of an external medium or folder.

Click the **Add to View** button to add this data to an ongoing session.

This way you can, for example, load a previous study from a patient medium (CD or DVD) to compare it with a current study, which you have already loaded from your database.

Only active on a DICOM node tab and only for users with permission to query and retrieve data from a remote DICOM node.

Select data on a DICOM node and click the **Retrieve** button to copy this data to the database. You can subsequently load the data onto the **View** window from there.

Only active on the Database tab and only for users with delete permission.

Select one or several studies or series in the study/series list of the local database and click **Delete** to remove this data from the database.

If a patient, study or series is displayed dimmed (grayed out) in the local study/series list, this means that the data cannot be loaded onto the **View** window. The data can still be deleted.

You cannot delete data on remote servers.

Session management

Visage 7 Client supports session management. This means that you can save processing and evaluation results before you end a session (for example when you load new data or close the program). When you return at a later time, you can load the session again and resume your work or present your results to colleagues.

Note

Session information is temporary data. Sessions are stored on the Visage server as long as the studies they refer to are stored on the server. Once a patient or study is deleted from the database, session information is lost.
Deletion of patient and study data may be triggered manually or automatically, when the hard disk is full. Automatic deletion of study data affects the oldest studies on the server.

If session management has been enabled for your user account, the lower right-hand corner of the **Study Browser** displays a session list.

Recent or study sessions

Use the **Show My Recent Sessions** button to show a list of your most recent sessions (for all studies) in the session management section of the Import window.

-Or-

Click a study in the study/series list to show only sessions of this study in the session management section.

Loading a session

Double-click a session in the session list to load its dataset(s) and session settings onto the **View** window.

Auto logoff session

If the system logs you off automatically (after an extended period of no user interaction) the currently loaded dataset(s) and all your preliminary processing and evaluation results are automatically saved in an **auto logoff** session.

An **auto logoff** session is shown in red and in the topmost position in the session management section of the **Study Browser** after you have logged on again.

Tip

Open the **auto logoff** session immediately after you have logged on again and decide whether to save it in a user-created session. When you are logged off automatically a second time, a new **auto logoff** session is created and the previous session is overwritten.

Session sharing

You can use session management to share your work with colleagues.

When saving a session, the system prompts you to indicate if you want to save this session under your own user name or if you want to share it with other users. Ses-

sions that you made available for all users are marked with **(shared)** in the session management box of the **Study Browser**.

Shared sessions can also be sent as session links to colleagues via email. When your colleagues receive such emails, all they need to do is to double-click the attached link to open the Visage 7 Client and display this session.

Note
Sharing sessions via email requires that the Visage 7 Client has been installed on recipients' computers before they click the email link.

Tip
Remember to save recent changes (**File > Save Session**) before sending a session link (**File > Email Session Link**).

Preview images

When a dataset is selected in the local database, a preview is displayed automatically in the preview area. In case of 3D datasets, this preview displays the central slice. If multiple series are selected, a preview image is shown for each of these series.

On remote DICOM nodes, previews are available only if the selected series has already been sent to the Visage server.

If a session is selected in the session management section, a screenshot of the **View** window is shown in the preview section. The screenshot shows the **View** window with the session data at the time when the session was saved.

Windowing preview images

For a better overview, you can window preview images:

Click a preview image, hold the mouse button down, and drag the mouse up/down to change the window center or brightness, or right/left to change the window width or contrast.

Resizing the preview area

You can change the size of the preview window area and the study/series list by dragging the "split bar" that separates these window areas up or down.

You cannot resize individual preview images.
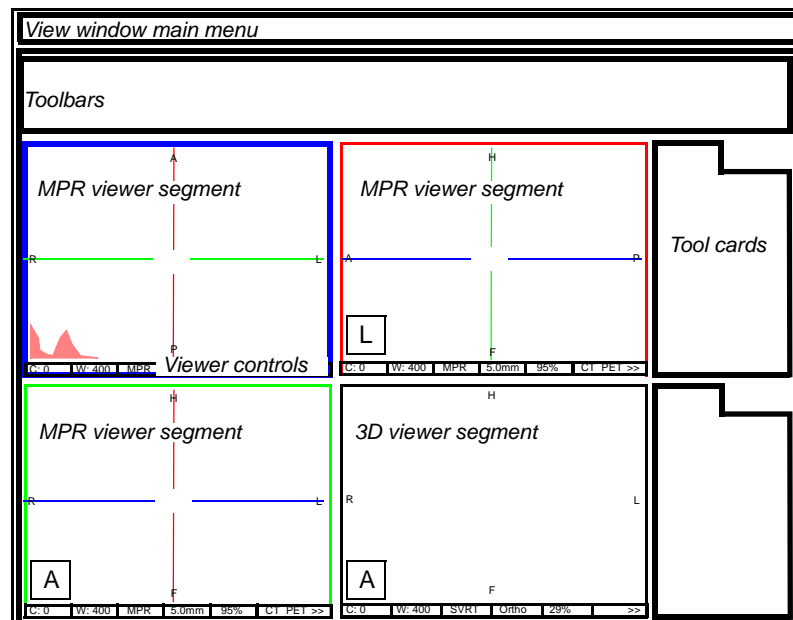
View Window

 You use the **View** window to display images and evaluate image information.

Window layout

Depending on your selection of data, the **View** window will be shown with a different window layout. This window layout is defined in a so-called "protocol".

The system will preselect a different protocol for data of different modalities and anatomical regions and depending on the monitor configuration and how many series you load onto the **View** window at a time. If you prefer another protocol you can select a different one from the **Protocol** menu.

Overview of the user interface

Protocols

Protocols define the layout of the **View** window and the display parameters for the loaded images.

Protocol assignment   When a user loads one or several studies, series, or volume datasets onto the **View** window the system automatically selects a suitable protocol to display the data. Depending on the system and protocol configuration the system uses a combination of several matching criteria to select the protocol best-suited for the loaded data.

- **Monitor configuration**

    Different protocols can be defined for different combinations of monitors and screen resolutions.

- **Study and series criteria**

    Protocol matching criteria usually include the modality or combination of modalities that acquired the data. For example, a CT series may be shown with a different window layout than an MR series or a combination of a CT and a PET series. Other study or series criteria may include the study description or part of the body that was examined or whether current and prior studies are being loaded onto the **View** window.

- **Protocol access and protocol ranking**

    Protocols may have been defined in such a way that they are available for individual users or user levels only. Moreover, protocols can be assigned priority ratings by users. A protocol with a high priority rating is more likely to be automatically selected than a protocol with a low priority rating.

Protocol definition   A number of protocols have been predefined for your system. Users with advanced user privileges can adapt these protocols and their matching criteria or create protocols of their own.

See *Visage 7 Client configuration* (*Protocol configuration*).

A protocol typically defines the following layout aspects:

- The number of image segments (viewers)

- The initial rendering parameters for each viewer

- The linking of viewer segments for synchronized navigation in multiple viewers

- The availability and location of toolbars

- The availability and location of tool cards

Changing the View window content   Each protocol defines one or more so-called layouts, so you can switch between different representations of the currently loaded data (see also *Layouts toolbar*). If the desired representation does not exist in the current protocol, you can select and apply a different protocol from the **Protocol** menu.

There are additional ways to change the images and display parameters in the View window:

Change the arrangement of viewer segments and load image data into these viewer segments manually.

See also *Interactive arrangement of viewer segments and image data*.

-Or-

Select different rendering parameters for MPR viewer segments or the 3D segment from the context menu or from the viewer controls.

See also *Viewer controls*, *3D viewer context menu*, and *MPR viewer context menu*

-Or-

Select additional tool cards from the **Tools** menu.

See also *View window main menu* and *Tool cards*

-Or-

Add toolbars to the toolbar section.

See also *View window main menu* and *Toolbars*.

Viewer segments

The Visage 7 Client **View** window is subdivided into several viewer segments. For example, if you have loaded a single thin slice CT dataset, it may be presented using three *MPR viewer segment*s and one additional *3D viewer segment*. The active viewer segment is indicated by a highlighted viewer frame.

Tip

Show crosshairs in all viewer segments. This will help you identify the position and orientation of the displayed slices in one MPR viewer with respect to the slices in the other MPR viewers and the 3D viewer segment.
See *3D viewer context menu* and *MPR viewer context menu* for how to enable crosshair display.

Linked viewers   Viewer segments can be linked, which means that image manipulation steps are automatically applied to all linked viewer segments and not only to the one that was active when you made the changes. As a rule, all MPR viewer segments that show images from the same dataset are linked. Linking of viewers is defined in the currently active protocol.

Linking affects one or several image manipulation steps, depending on how linking has been defined in the protocol. For example, slice browsing is synchronized in all viewers that have been linked in a translation group, and zooming is synchronized in all viewer segments that belong to the same zoom group. Users can edit the ways in which viewers are linked, either for the duration of an entire session or only temporarily for the next image manipulation step. Use *Attach/Detach Viewer* or *Edit*

Viewer Linking from the viewer segment context menu or the *Viewer Linking tools* to change the way viewers are linked.

Image text and warning symbols

Aside from image information, the viewer segments contain information about the loaded data in the form of image text and icons.

The following symbols in images alert you to the fact that an image is shown with reduced image quality or that warnings exist concerning the displayed images.

Low resolution warning

A red bullet in the lower right-hand corner of a viewer segment indicates reduced image quality. The low resolution warning may appear while the dataset is still being loaded and the system generates full image quality, or if a low streaming compression level has been selected.

Image processing in progress

A yellow bullet in the lower right-hand corner of a viewer segment indicates that the image shown in this viewer has not yet been updated with your latest image processing step. The previous image is still displayed while image processing is performed in the background. As soon as image processing is complete and the image display has been updated the yellow bullet disappears.

Note

Do not use images that show a red or yellow bullet in the lower right-hand corner of the viewer segment for primary diagnosis. Wait until the bullet has disappeared (see also *View window main menu*).

Miscellaneous warnings

A yellow warning triangle in the upper left-hand corner of the images indicates that warnings exist for this dataset.

Caution

Find out more about these warnings by clicking the yellow warning triangle if it is shown in your viewers.

Scale

For calibrated image types (e.g. CT images) a scale can be shown on the right edge of the viewer segments. The scale looks like a small ruler and indicates centimeters or millimeters when you zoom in on an image.

Showing/hiding image text

If the image text is in your way during image processing, you can either hide it altogether or hide selected blocks of text information.

Use **View > Show in Viewer > ...** in the main menu to hide or redisplay specific blocks of image text in all viewer segments.

-Or-

Use **View > Show in Viewer > Toggle All** or the keyboard shortcut **Spacebar** to hide or redisplay all image texts in all viewer segments.

Viewer controls   Each viewer segment has a number of controls within easy reach along its lower border. You can use these controls to toggle or select display options relevant for this viewer segment.

Click the arrow icon to the right of a viewer control to drop down a selection list.

-Or-

Click a value and overwrite it to change the window center/width, slice thickness or zoom percentage of images, for example.

3D viewer segment

The 3D viewer segment displays a 2D projection of a 3D volume.

You can choose between several volume rendering techniques and display modes in the 3D viewer segment.

In the 3D viewer segment you can rotate this image in order to generate arbitrary 3D views, and you can zoom or pan the image and adjust window/level. Use the viewer controls, the mouse, the 3D viewer context menu, or toolbar icons to do so.
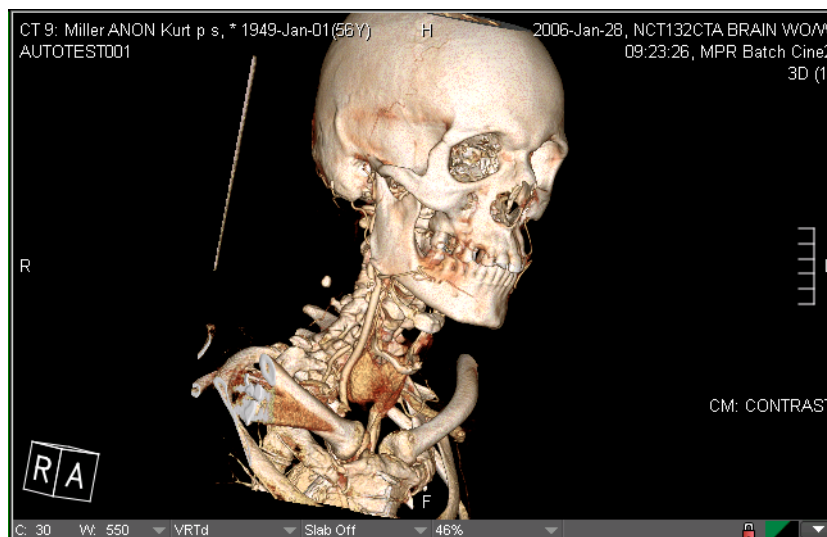
3D rendering techniques in the 3D viewer

Choose one of these 3D rendering techniques from the 3D viewer controls or the 3D viewer context menu:

- **3D MIP**

  Maximum intensity projection: Visage 7 Client calculates the *maximum* of all the voxel values lying on the virtual viewing ray behind this pixel. 3D MIP requires a grayscale color map.

- **3D MIP (inverse)**

  Similar to MIP, but displayed inversely (black on white instead of white on black).

- **VRT**

  Volume rendering technique, also called emission-absorption model: This technique maps data values to colors and transparencies defined in a 3D color map. The voxels are interpreted as small diffuse light sources emitting and absorbing light in the direction of the viewer. Each voxel is interpreted as a local diffuse light source, without additional shading.

  See also *3D Color Map tool card (3D viewer)* and *Templates tool card (3D viewer)*.

- **VRT (diffuse)**

  Similar to VRT, however, an additional virtual light source and a diffuse lighting model is used to add shades to the visual surfaces of the volume. For example, curved surfaces become darker towards the edges, which results in a more natural appearance.

- **VRT (specular)**

  An addition to diffuse shading, specular shading uses a lighting model that reflects light dependent on the angle between the incoming and reflected light.

This means that on smooth surfaces the user will see highlights, and that the shading becomes even more expressive than with diffuse shading. Specular shading is especially good for large surfaces with fine detail.

Projection modes in the 3D viewer

Choose one of these projection modes for the 3D image from the viewer controls:

- **Orthographic**

  Orthographic viewing is like viewing an object through a lens with a very long focal distance (telelens), where the viewing rays are almost parallel to each other, and no perspective distortion occurs.

- **Perspective**

  This display mode gives a more natural impression. It corresponds with the everyday experience of perspective distortion. Objects that are far away appear smaller than objects close by.
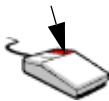

Tip

In orthographic mode you can perform 2D measurements in the image plane (e.g. distance and angle measurements). In perspective mode this is not possible.

3D viewer context menu

The 3D viewer context menu provides quick access to functions. Some of these functions are also available from toolbars or tool cards while others can be selected in this context menu only.

Tip

Refer to the *Toolbars* section for an explanation of all context menu entries with a small icon or image in front of them.

Right-click in a viewer segment to show the context menu.

-Or-

Use this control in the viewer control bar to call the context menu.

**3D viewer context
menu options**

Fullscreen	Select this menu option or double-click in the 3D viewer segment to display the 3D viewer in full screen mode.
	Select the command or double-click again to return to the previous screen layout.
Viewer Control	Check or uncheck this commands to show or hide the viewer controls bar below the 3D viewer segment.
View Study Reports	If a study report has been sent to the Visage from the RIS, you can show this report in a separate window with this command.
Store Key View	Stores what is currently shown in the 3D viewer segment as a key view. During your session you can return to this view using the *Recall Key View* menu entry or by pressing F11/F12 (*Previous/Next Key View*).
	Note that key views are lost when you close Visage 7 Client or load new data. To preserve key views save your session (*File > Save Session* or *File > Save Session As*).
Recall Key View	Allows you to select and redisplay one of the stored key views.
Delete Key View	Allows you to delete a key view you created earlier during your session.
Crosshair	Shows or hides a 3D crosshair showing the orientation and position of the slices currently shown in the MPR viewer segments in the 3D viewer.
Bounding Box	Shows or hides a box delineating the volume borders in the 3D viewer.
Centerline	Turns on display of the centerline for vessel segmentation for this viewer segment.
View Orientation	Opens a submenu with commands for rotating, flipping and centering the displayed volume.
Properties	Opens a submenu with alternative display options for the selected viewer segment.
	Use this submenu to change the rendering technique in the 3D viewer segment, for example (see also *3D rendering techniques in the 3D viewer*).
	Or use this submenu to select **Smart Sampling**, which reduces artifacts in the volume display, or to toggle between orthographic and perspective display (see also *Projection modes in the 3D viewer*).
Attach/Detach Viewer	Opens a submenu in which you can detach, which means temporarily remove, a viewer from a linked viewers group.
	-Or-
	Select **Edit Viewer Linking** in this submenu to enter viewer group editing more. In this mode icons that represent groups of image manipulation tools are shown in the various viewer segments. You add a segment to a group by selecting the corresponding tool icon in a viewer segment. End this more by confirming your selection (checkmark icon in the lower right-hand corner of the last viewer segment in which you have clicked a tool group icon).

MPR viewer segment

An MPR viewer displays slice images.

• Original scan images belonging to a 3D volume created by a postprocessing application (single MPR viewers only, but not for viewers of an MPR crosshair group).

-Or-

• Reconstructed arbitrary slices through a volume dataset.

  Immediately after loading a dataset and depending on the currently active protocol, the MPR viewer segments show slices of the standard anatomical views.

In the MPR viewer segments you can perform various image manipulation and evaluation procedures, such as changing image display parameters and using measurement and annotation functions. Use the viewer controls, the mouse, the MPR viewer context menu, or toolbar icons to do so.


Tip

MPR viewers showing the same image series are implicitly linked. When you change display parameters in one MPR viewer segment, all MPR viewers showing images from the same series will be updated as well.

When you have loaded a volume dataset, you can use the MPR viewer segments to create new slice images by moving and rotating the navigation crosshair.

You can change the slice thickness and choose a different compositing technique for your images.

If you have loaded suitable volume data (i.e. two series of volume datasets from the same study) you can toggle between the primary and overlay dataset, activate fusion mode, and fade between the primary and the overlay dataset.
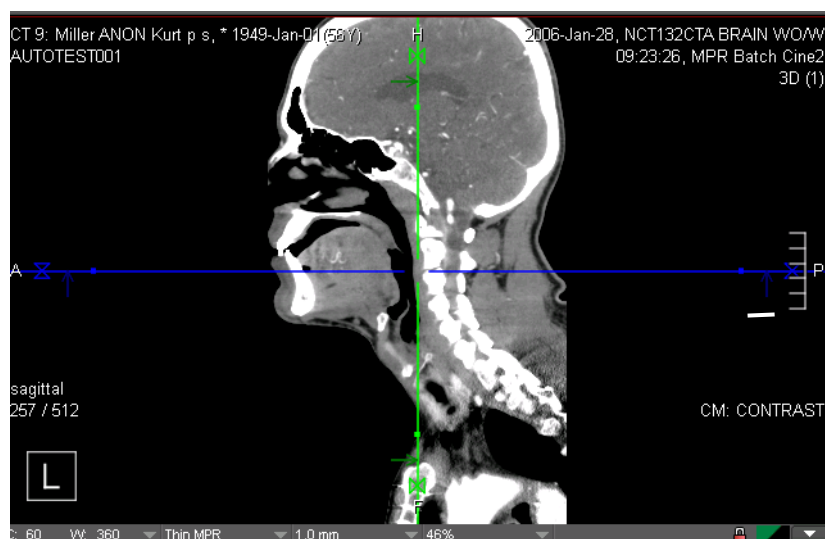
Navigation crosshair

For volume datasets the navigation crosshair in an MPR viewer segment indicates the orientation and position of the slices that are currently shown in the two other MPR viewers for this dataset.

- A **blue** line represents the image currently shown in the MPR segment with the blue viewer frame.

- A **green** line represents the image currently shown in the MPR segment with the green viewer frame.
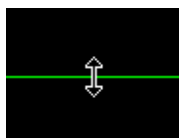
- A **red** line represents the image currently shown in the MPR segment with the red viewer frame.

	Small arrows pointing to the crosshair indicate the viewing direction in the other two MPR viewer segments.
	When you move the cursor over the center of the crosshair, the cursor changes shape. Click and drag the entire crosshair. This moves two view planes simultaneously in the volume dataset and shows new slice images in both of the other MPR viewer segments. Note that the move cursor is not available for *Partial Crosshair* display.
	When you move the cursor over a crosshair line, the cursor changes shape. Click and drag this line up or down. That will take you through the volume dataset along the two other standard axes and update the view in one of the other MPR viewer segments.
	When you move the cursor over the rotation handles (small dots), the cursor changes shape. Click and drag the cursor up or down to rotate the navigation crosshair. This updates the views in the two other slice segments, and generates slice images with non-standard views.
	When you click one of the small triangles on the crosshair lines along the edges of the image the crosshair lines are shown dotted. You can now change the slice thickness in the MPR viewers by dragging the slice thickness handles up or down. As soon as you release the mouse button the slice thickness indicator and the selected thick slice compositing mode are updated in the viewer controls.

Tip

Also show the crosshair in the 3D viewer segment while you navigate through your volume with the navigation crosshair in the MPR viewers. See *3D viewer context menu* for how to enable crosshair display in the 3D viewer segment.

Compositing modes for thick slices

The default slice thickness for reconstructed images in MPR viewer segments is specified in the active protocol. It is usually the slice thickness of the original scans.

You can change the slice thickness for your loaded images and subsequently choose a different compositing technique for thick slices.

- **Thin MPR**

  In this mode slices are shown in their original ("native") thickness.

- **Maximum intensity (MIP)**

  Data values are computed as the *maximum* of the values of the original slices.

- **Minimum intensity (MinIP)**

  Data values are computed as the *minimum* of the values of the original slices.

- **Average intensity (AvIP)**

  When displaying a thick slice, data values are computed as the average of the values of the original slices.

You work with the *Viewer controls* or the *Display tool card* when changing the slice thickness and selecting a different compositing technique.

-Or-

Use the keyboard shortcut **T** to turn thick slice display on and off.

MPR viewer context menu

The MPR viewer context menu provides quick access to functions. Some of these functions are also available from toolbars or tool cards while others can be selected in this context menu only.
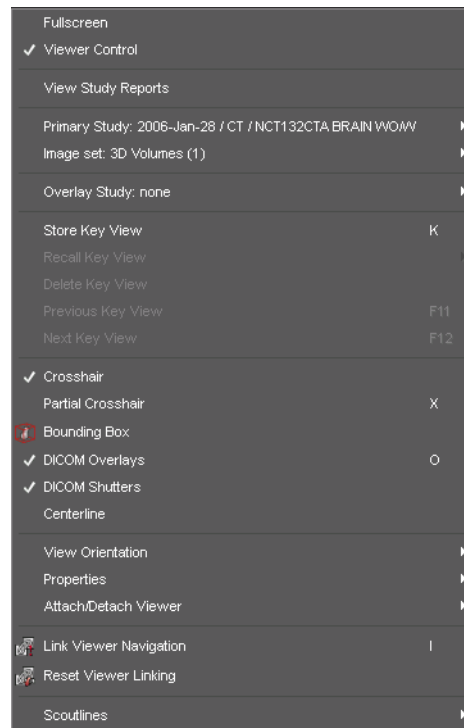
Right-click in a viewer segment to show the context menu.

-Or-

Use this control in the viewer control bar to call the context menu.

MPR viewer context menu options

Fullscreen	Select this menu option or double-click in the MPR viewer segment to display the MPR viewer in full screen mode.
	Select the command or double-click again to return to the previous screen layout.
Viewer Controls	Check or uncheck this commands to show or hide the viewer controls bar below MPR viewer segments.
View Study Reports	If a study report has been sent to the Visage from the RIS, you can show this report in a separate window with this command.
Select As Baseline Phase	*Only for time series.*
	Defines the current phase image as baseline phase. In a time-series analysis, this defines which image will be subtracted from all the other images in the time series.
Store Key View	Stores what is currently shown in the currently active (highlighted) segment as a key view. During your session you can return to this view using the *Recall Key View* menu entry or by pressing F11/F12 (*Previous/Next Key View*).
	Note that key views are lost when you close Visage 7 Client or load new data. To preserve key views save your session (*File > Save Session* or *File > Save Session As*).
Recall Key View	Allows you to select and redisplay one of the stored key views.
Delete Key View	Allows you to delete a key view you created earlier during your session.
Crosshair	Shows or hides the navigation crosshair in MPR viewer segments.

|	
Partial Crosshair	Shows or hides a section in the middle of the navigation crosshair, which might be in the way when reviewing images.
	Note that when this option is selected, you cannot move the entire crosshair (the cursor will not change shape when you point to the crosshair intersection; see also *Navigation crosshair*). You can, however, move single crosshair lines.
	Advanced users can toggle display of the partial crosshair via keyboard shortcut (key **X**).
Bounding Box	Shows or hides a box delineating the volume borders in the MPR viewer segments.
DICOM Overlays	If a dataset contains DICOM overlays use this context command to show or hide them.
DICOM Shutters	If a dataset contains DICOM shutter information use this context command to show or hide the shutter.
DICOM Annotations	If a dataset contains DICOM annotations use this context command to show or hide them. DICOM annotations are more comprehensive graphic and text annotations than DICOM overlays and they are stored in DICOM presentation states.
Centerline	Turns on display of the centerline for vessel segmentation for this viewer segment.
DICOM Print	Starts a DICOM print action either for the current image or image set. You can select the DICOM printer you want to use as well as layout and media properties.
View Orientation	Opens a submenu with commands for rotating, flipping and centering images.
Properties	Opens a submenu with alternative display options for the selected viewer segment.
	Use this submenu to toggle between thin or thick slice display and to switch between compositing modes for thick slices (see also *Compositing modes for thick slices*).
	Also use this submenu to select **Bilinear Filtering**, which interpolates MPR rendered slices for a smoother appearance or to show or hide **Slice Boundaries**.
Attach/Detach Viewer	Opens a submenu in which you can detach, which means temporarily remove, a viewer from a linked viewers group.
	-Or-
	Select **Edit Viewer Linking** in this submenu to enter viewer group editing more. In this mode icons that represent groups of image manipulation tools are shown in the various viewer segments. You add a segment to a group by selecting the corresponding tool icon in a viewer segment. End this more by confirming your selection (checkmark icon in the lower right-hand corner of the last viewer segment in which you have clicked a tool group icon).
Scoutlines	If several series are loaded which show the same anatomical region (same frame of reference) but from a different orientation you can show the location of images of one series in the images of the other series as scoutlines.

2D viewer

The 2D viewer displays original slice images such as the scan images of a series or a topogram.

Depending on the active protocol, the 2D viewer may be shown in a viewer segment, which replaces one of the other segments or the 2D viewer is shown fullscreen.

> **Tip**
>
> The 2D viewer allows you to scroll though a large number of images quickly. Advanced image processing and analysis functions are not available in the 2D viewer (these functions are only available in MPR viewer segments). Image manipulation tools that do not make sense for original scan images are dimmed in the toolbar section of the 2D viewer.

Any image manipulation and evaluation options available in the 2D viewer can be accessed via mouse keys, toolbar icons, or the 2D viewer context menu.
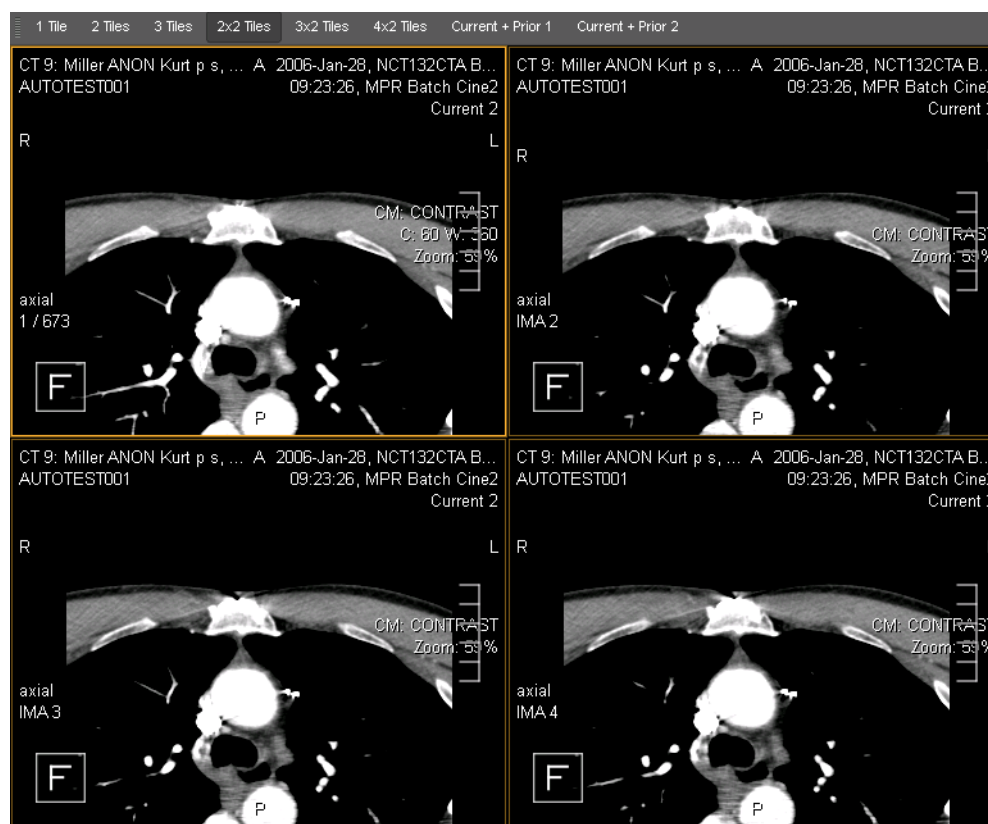
Layouts toolbar   Use the **Layouts** toolbar, which is usually shown above the 2D viewer segment, to select how many images you want to show in the 2D viewer segments.
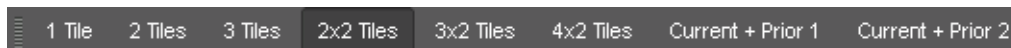
If the **Layouts** toolbar is not currently shown, select it from the context menu of the toolbar section or from the **View > Show Toolbars** submenu.

Interactive arrangement of viewer segments and image data

When you load image data onto the **View** window a protocol is automatically selected. This protocol defines the arrangement of viewer segments and which images or volume data are shown in these segments.

In order to adapt the arrangement of image data interactively you use the *Layout toolbar* and the *Image Series tool card.*

Layout toolbar

If the **Layouts** toolbar is not currently shown, select it from the context menu of the toolbar section or from the **View > Show Toolbars** submenu.

The **Layouts** toolbar offers you alternative arrangements of viewer segments which have been defined for the currently active protocol.

Click on of the buttons in this toolbar to show a new arrangement of viewer segments on the View window.

Image Series tool card

The **Image Series** tool card is usually shown along the bottom of the window. It contains thumbnails of all the currently loaded studies, series, images and volume datasets. It can be opened using the arrow button if it is not opened automatically.
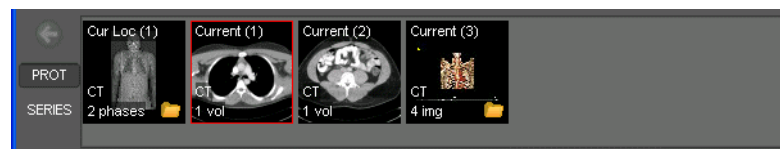
Loading image data   Use the thumbnails to load volume datasets, 2D images, or image stacks into the various viewer segments.

Click a thumbnail and drag it onto a viewer segment to replace the images in this and any other viewer segments that shows orthogonal slices or the 3D display of this dataset.

-Or-

Right-drag the image into a viewer segment in fusion mode in order to define this dataset as the overlay dataset. (Use the viewer context menu to undo this setting.)

Folder icon

If a thumbnail represents several volume datasets, images in a series, or phase images this is indicated by a small folder icon in the lower right-hand corner of the thumbnail.

Double-click the thumbnail with the folder icon to show the volume datasets or images it contains.

Use the **Go back** icon (green arrow) to return to the dataset overview display.

Protocol or series mode

Use these two buttons to toggle the display mode of the **Image Series** tool card:

- **PROT** - shows all image series in the current protocol.
- **SERIES** - shows all loaded series of all loaded studies according to their DICOM hierarchy.

Mouse operation

Advanced Visage 7 Client users can perform many of the most frequent image manipulation tasks directly in the viewer segments with the left, middle, or right mouse button. This way you do not have to move the mouse to activate or switch tools.

To operate Visage 7 Client primarily with the mouse you need to distinguish between clicking and dragging.

Visage 7 Client has functions assigned to clicks with the left, middle, or right mouse button.

Dragging implies clicking the left, middle, or right mouse button, and moving the mouse while you hold the mouse button down.

If your computer is equipped with a wheel mouse you can use it for scrolling by turning the wheel, or you can click the wheel, this way it functions as the middle mouse button.
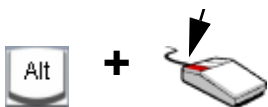
Some functions require that you keep the **Shift**, **Ctrl**, or **Alt** keys on your keyboard pressed while you click or drag the left, middle, or right mouse button.

The following tables list all functions assigned to mouse buttons, combinations of mouse buttons, and combinations of keys plus mouse buttons.

Single mouse button

Left-click	Selects a viewer segment or performs a function (i.e. the function selected by the currently active tool).
Left-drag	Performs the default navigation function of the currently active viewer segment, or the function of the currently active tool.
Middle-drag	Zooms the images in all linked viewers: Move the mouse up to zoom in, or move the mouse down to zoom out
Mouse wheel	Browses through the image stack in the MPR viewer, CPR viewer, lumen viewer, or 2D viewer segments.
Right-click	Selects a viewer segment and calls up the viewer context menu, or calls up the context menu of any other window section or control for which a context menu exists. -Or- Selects or activates a control for which no context menu exists.
Right-drag	Pans the image, i.e. moves the image in the viewer segment.

Two mouse buttons

Left + right-drag	Changes window levels in all viewers linked for joint windowing: Move the mouse up or down to change the window center (brightness) Move the mouse left or right to change the window width (contrast)
Middle + right-drag	Browses through the image stack in the MPR viewer, CPR viewer, lumen viewer, or 2D viewer segments. *This mouse button combination is not active in the 3D viewer segment.*

Shift key + mouse button

Shift + left-drag	Changes the segmentation threshold in lesion segmentation mode.
Shift + middle-drag	Zooms only the image in the selected viewer segment in or out. (Leaves images in linked viewers unchanged).

Control key + mouse button

Ctrl + left-drag	Always performs the default navigation function of the currently active viewer segment regardless of the currently active tool.

Alt key + mouse button

Alt + left-click	*Position Crosshair (F7)*: moves the crosshair center in all viewer segments to this point. This updates all MPR viewer segments that show this dataset.
Alt + left-drag	*Position Crosshair (F7)* (see above).
Alt + middle-drag	Changes the slice thickness when you perform this action in an MPR viewer segment. -Or- Selects the *Crop Slab* tool and changes the slab thickness if you perform this action in the 3D viewer segment.

Mac users   Generally, mouse operation for Mac users is the same as described above, with the Ctrl key replaced by the Cmd key. However, in order to use these functions, you should apapt the mouse settings to distinguish left and right mouse button via **System Preferences > Mouse**.

> **Note**
>
> Some types of mice, such as the Mighty Mouse and Magic Mouse from Apple, do not support pressing the left and right mouse button together. In this case, window levels have to be changed by activating the W/L Tool.

Toolbars

A number of icons are shown along the edges of your window after you have loaded data. With these icons you can start functions or select options with a single mouse click. The icons are grouped in toolbars. Which toolbars are shown when you first load data as well as the toolbar position depends on the currently active protocol.

If you wish, you can change the arrangement of toolbars for the duration of your current session. You can show more toolbars or hide toolbars currently shown, or you can change the location of a toolbar by dragging it across the window and dropping it wherever you prefer it to be shown. When you drag a toolbar to the left, right or bottom edge of the window a new toolbar section appears there. When you drag and drop a toolbar anywhere else on the window it is shown in a floating window.

Some of the functions and options that are represented by toolbar icons can also be called up with keyboard shortcuts. These keyboard shortcuts are active even if a toolbar or icon is currently not displayed in any of the toolbar sections on the window.

Tip

A number of keyboard shortcuts have been predefined for the Visage 7 Client. These keyboard shortcuts are indicated in brackets after the function name in the tool description tables in this user manual. Or select **Help > Keyboard shortcuts** in the main menu to show a list of these keyboard shortcuts.
Note, however, that users with appropriate user rights can change the assignment of keyboard shortcuts for their own user account or on a system-wide basis (see also *Visage 7 Client configuration* (*Keyboard Shortcuts*). This means that the keyboard shortcuts list in the main menu as well as the keyboard shortcuts indicated in this user manual may no longer be correct for your system.

Working with toolbar icons

Tool tips   All icons are assigned tool tips. A tool tip explains the function of an icon.

Position the mouse cursor on an icon and let it rest there for a short time.

A brief explanation of this icon appears.

Active function   Some icons start functions immediately, others allow you to activate a processing mode.

When a processing option is selected and therefore active the corresponding icon is displayed with a gray background.

Drop-down icon bars

Some icons represent a drop-down icon bar. This is indicated by a small triangle pointing downwards.

1. Click exactly on the small triangle in the lower right-hand corner of a drop-down icon.

   -Or-

   Click a drop-down icon and hold the mouse button pressed for a little while.

2. Move the mouse cursor along the icon bar until it points to the function or image processing tool you wish to select.

3. Click an icon on the drop-down icon bar to select this function or option.

   For frequently used functions the program now replaces the drop-down icon in the toolbar with the icon you last selected. This makes it the preferred icon in this drop-down icon bar. The next time you wish to activate this function all you have to do is click this icon, you no longer have to drop down the icon bar.

   Icons that represent rarely used functions will stay in the drop-down icon bar and not move up to the top level.

Showing or hiding toolbars

If the currently displayed selection of toolbars does not contain the icon or icons you are looking for, you can show more toolbars.

Use **View > Show Toolbars** in the main menu to show or hide toolbars.

-Or-

Right-click in the toolbar section of the window to open a menu with all available toolbars. Check additional toolbars here.

Standard tools

Toolbars group icons by function, frequency of use, and suitability for specific datasets and diagnostic problems. Which toolbars are available after you have loaded your data depends on your active protocol and on your general configuration. The active protocol defines which toolbars are shown directly after you have loaded data and also which toolbars are available in the first place.

This user manual describes the standard toolbars of the Visage 7 Client and the tools these toolbars contain. In addition to these standard toolbars you may find additional toolbars with icon groups that were defined for a specific protocol.

Navigation tools

Default Navigation (F1)

The default navigation tool is set to browse slices when the active viewer segment is an MPR, CPR, lumen or 2D viewer, and to 3D rotate when the active viewer segment is a 3D viewer.

> **Tip**
>
> With the **Ctrl** key you can return to the default navigation tool temporarily. Default navigation will be active for as long as the **Ctrl** key is pressed. When you release the key you return to the currently selected program function.

3D Rotate (F2)

3D viewer segment: Click anywhere in the viewer segment, hold the mouse button pressed, and drag the mouse to rotate the 3D volume in the direction of the mouse movement.

Use any of the standard orientation icons or keyboard shortcuts (*Anterior (A), Posterior (P), Left (L), Right (R), Head (H), Foot View (F)*) to reset rotation.

MPR viewer segments: Click the point in the image that is to be the center of rotation. Hold the mouse button pressed, and drag the mouse to rotate the image plane. New slice images in non-standard orientations are created in the process. If the orientation labels and orientation cube are currently shown in a segment, they indicate the new image orientation.

Use *Reset Slice Orientation (F9)* to return to the original image orientation.

Pan (F3)

Select this icon and click and drag the mouse across an MPR viewer or 3D viewer segment to move the image within the segment.

Zoom (F4)

Select this icon, click in a viewer segment, hold the mouse button pressed, and drag the mouse cursor up to zoom in, or down to zoom out. Or use the percentage box in the viewer controls to change the image display size.

Window Level (F5)

Select this icon, click a viewer segment, hold the mouse button pressed, and drag the mouse cursor left/right to change the window width (contrast), or up/down to change the window center (brightness).

While the **Window Level** tool is active in a viewer segment, a histogram of grayscale values is also shown in the lower left-hand corner of the segment. A small white bar that moves as you shift the window center and expands or shrinks when you change the window width indicates the current window settings graphically.

Note that when you window an image segment in fusion mode this will affect the window values of the primary dataset. In order to window the image of the overlay dataset, hold the **Shift** key pressed while you window the image.

Browse Slices (F6)

The browsing tool allows the use of the mouse to navigate through an image stack in an MPR viewer. Select this icon, click a viewer segment, hold the mouse button pressed, and drag the mouse cursor up/down to scroll forward or backward through the image stack.

Position Crosshair (F7)

Select this icon and click a visible (opaque) structure in the 3D viewer or any point in one of the images in the MPR viewer segments. This sets the crosshair cursor of the MPR viewers to this 3D position and updates all MPR viewer segments that show this dataset.

Orientation tools

Anterior (A), Posterior (P), Left (L), Right (R), Head (H), Foot View (F)

Displays the volume in the 3D overview segment or a slice image in one of the MPR viewer segments in the standard anatomical views anterior, posterior, left, right, head, or feet.

Image size tools

Zoom 100%

Clicking this icon represents every pixel in the image as a pixel on the window, thus representing the image "as is".

Fit Width/Height, Fit Width, Fit Height

Select one of these icons while a 3D viewer segment is active to resize the displayed 3D volume so that it fits optimally in the segment (**Fit Width/Height**), or so that it makes optimum use of the segment width (**Fit Width**) or segment height (**Fit Height**).

-Or-

Select one of these icons while an MPR viewer segment is active to resize the images in this and all other linked MPR segments in one go.

Rotate/Flip Images tools

Rotate Clockwise, Rotate Counterclockwise

Select one of these icons while an MPR viewer is active to rotate the image in the active viewer segment by 90° clockwise or counterclockwise. Rotation is applied only to the segment in which you clicked (3D viewer or MPR viewer).

Flip Horizontally, Flip Vertically

Select one of these icons while an MPR viewer is active to rotate the currently displayed image around its vertical or horizontal axis.

Note that you cannot flip the 3D volume in the 3D viewer.

Dataset Navigation tools

Previous Study, Next Study

If you have loaded more than one 3D study, use these icons to scroll through the loaded studies.

Previous Volume or Muliframe Image (Ctrl + ⬅), Next Volume or Muliframe Image (Ctrl + ➡)

If more than one 3D volume is assigned to an MPR or 3D viewer, or more than one multiframe image is assigned to a 2D viewer, use these tools to switch between the different objects assigned to the viewer.

Previous Phase of Time Series (⬅), Next Phase of Time Series (➡)

If you have loaded a time series, use these icons to scroll through the phases.

Annotation and Measurement tools

With these tools you can annotate and evaluate image information in slice images (MPR viewers) as well as in the 3D viewer. Note, however, that measurements in the 3D volume of the 3D viewer segment are only possible in orthographic but not in perspective display mode.

Saving annotations   For information about how to save annotations and measurements refer to *Saving annotations and measurements*.

Arrow/Text Annotation

Select this tool and click in an image segment to create a **text annotation**.

-Or-

Click in an image segment, hold the mouse button pressed, and drag the mouse across the image to create an arrow plus text annotation (straight line with arrow).

The **Edit Annotation** dialog box is automatically opened.

Subsequently, you can also right-click the arrow or annotation text and select **Properties** to open the **Edit Annotation** dialog box.

Refer to *Editing annotations* and *Edit Annotation dialog box* for information on how to move, edit, or format annotation texts.

Refer to *Showing annotation text at a fixed viewer position* if you want to freeze annotation text in a viewer segment.

Circle Annotation

Select this tool and click in an image segment to create a circle with a predefined radius.

-Or-

Click in an image segment, hold the mouse button pressed, and drag the mouse across the image to create a circle with your own radius. You can right-click the circle and select **Set Size as Default** to define this radius as your own default.

The **Edit Annotation** dialog box is automatically opened when a new circle is created.

Subsequently, you can also right-click the circle or annotation text and select **Properties** to open the **Edit Annotation** dialog box.

Refer to *Editing annotations* and *Edit Annotation dialog box* for information on how to move, edit, or format annotation texts.

Refer to *Showing annotation text at a fixed viewer position* if you want to freeze annotation text in a viewer segment.

Distance (D)

Select this tool, click where you want to start your distance measurement, hold the mouse button down, drag the mouse across the image, and release the mouse button at the end point of your distance line.

-Or-

Create a line that consists of several segments: start the first segment, press the **Shift** key before you release the mouse button at the end of the first segment. Hold the **Shift** key pressed while you draw the other segments. Release the **Shift** key before the last click.

The distance is indicated in mm (millimeters).

Display the *Line Profile tool card* tool for an intensity profile (or HU value profile for CT) of your distance line.

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

The accuracy of distance measurements is ± 2 pixels. Larger errors can occur if the image is displayed with reduced matrix size, that is if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be greater still.

Angle

Select this icon, click in an image segment, hold the mouse button down, and drag the mouse to draw the first leg of an angle. Click when you have reached the vertex and draw the second leg.

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

Angle (Two Lines)

Select this icon, click and draw two separate lines in your image. If the lines intersect the program calculates both the acute and the obtuse angle. If the lines do not intersect in the viewer segment the program calculates only the acute angle.

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

The accuracy of angle measurements depends on the length of the shorter of the two angle legs. The longer the angle legs are, the better the accuracy.
For example:
Length of shorter angle leg (measurement error):
10 pixels (± 12°), 20 pixels (± 6°), 50 pixels (± 2.5°), 100 pixels (± 1.1°)
Larger errors can occur if the image is displayed with reduced matrix size, that is if not every original pixel is shown on the window due to zoom-out. For optimum accuracy we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be greater still.

Distance Ratio

Click this icon and perform distance measurements. The system will display the length of the two distance lines and the ratio between the two measurements.

Vertical Distance

Click this icon and two points in the image. Visage 7 Client will draw two horizontal lines and measure the vertical distance between these lines.

Calibrate Image *(only in 2D images)*

Some image types have no aspect ratio information in their DICOM image header. For these images distances cannot automatically be expressed in millimeters. You can, however, calibrate the distance tool using known distances in images (e.g. image markers or the length of a ruler).

Click this icon and measure a known distance. Enter that distance (in millimeters) in the **Calibrate** dialog box.

Elliptic ROI

Click this icon and draw an elliptical ROI. The ROI area is indicated in mm² (square millimeters).

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

Caution

The relative error of the elliptical ROI measurement is ± 2 pixels/(shorter radius). For example:
Shorter radius (measurement error):
10 pixels (± 20%), 20 pixels (± 10%), 50 pixels (± 4%), 100 pixels (± 2%)
Larger errors can occur if the image is displayed with reduced matrix size, that is if not every original pixel is shown on the screen due to zoom-out. For optimum accuracy we recommend zooming into the structure of interest as much as possible. The accuracy is further limited by the physical resolution of the acquisition itself. If the monitor used for display does not permit exact pixel selection, the inaccuracy can be greater still.

Circular ROI

Click this icon and draw a circular ROI. The ROI area is indicated in mm² (square millimeters).

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

Spherical ROI

Click this icon to draw a spherical ROI in a 3D dataset. When you release the mouse button statistics for both the diameter and the volume of the sphere are shown.

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

Point-Sized ROI

Select this icon and click a point in an image to show the density value as a measurement graphic, which you can save in a key view or snapshot.

Refer to *Editing annotations* for information on how to move or edit measurement graphics.

Pixel Value

Select this icon and move the mouse over an image in an MPR viewer segment. The pixel value of the cursor position is shown as image text in the lower left-hand corner of the viewer segment. The value changes as you move the mouse.

In CT images the pixel value is given in HU (Hounsfield Units). In other image types the units depend on the information stored in the DICOM data.

Cobb's Angle

With this tool you can measure Cobb's angles in spine datasets. Or use this tool to measure the angle between lines that intersect outside the visible image area.

Editing annotations

You can modify an annotation or measurement even after you have finished drawing it.

Click the annotation graphic to reselect it, and move the entire graphic.

-Or-

Move an end point of a line by clicking and dragging it to a new position.

-Or-

Right-click an annotation or measurement graphic and select **Properties** from the context menu to edit display properties.

-Or-

Delete the annotation graphic with the **Del.** key on your keyboard.

-Or-

Click a distance line that is in your way during image review. Hold the mouse button down, and drag the line to where it is no longer in your way. The end points of the original measurement are indicated as dots.

Note that a line profile cannot be shown for distance lines that you have moved as described here.

Edit Annotation dialog box

Double-click an annotation text to open the **Edit Annotation** dialog box.

Here you can overwrite the **Annotation** text, change the **Font Settings** for the annotation text, and select a color (**Set Color**) and **Line Width** for your annotation.

Selecting **Move Text Freely** allows you to move an annotation text independently of the annotation or measurement graphics.

With appropriate user privileges you can save your settings for future measurements and annotations in your user profile or on a system-wide basis. Click the **Default** button in the **Edit Annotation** dialog box to do so.

Showing annotation text at a fixed viewer position

1. Click the annotation text you want to freeze into this viewer segment for the current dataset.

2. Right-click and select **Fixed Position in Viewer** from the context menu.

   When you now start scrolling slices or change the orientation the annotation text will be shown in each slice image and at the same window position.

Note

Only text annotations can be frozen into a viewer segment this way. Arrow annotations and measurement graphics cannot be converted this way.

Saving annotations and measurements

Annotations and measurement graphics can be saved temporarily or permanently.

• Key view

Annotations and measurement graphics are automatically saved as key views. This means that when you scroll back to a slice during the same session your annotations and measurements will be shown again.

As soon as you close Visage 7 Client key views are lost unless you save them.

Tip

Use the **Recall Key View** item in the context menu of each viewer to return to a view in which you performed measurements or added annotations.

• Session management

You can save key views and other display settings in a session. Use *Save Session* or *Save Session As* from the main menu to do so.

• Snapshots

Use the *Snapshot Active Viewer (S)* icon to save your measurements and annotations in a snapshot. You can then insert a snapshot in your report or save it onto your hard disk.

Snapshot and Cine tools

Snapshot Active Viewer (S)

Creates a snapshot of the active viewer segment and places it on the **Export** tab card, where it will be available for reporting.

Snapshot All Viewers (Shift + S)

Creates several snapshot images, one for each image segment currently shown on the window.

-Or-

Combined Snapshot All Viewers - creates one snapshot which contains all image segments currently shown on the window.

Cropping tools

Use the cropping tools to cut away portions of the volume which hide more important information that lies underneath.

When you click a crop tool, orange lines appear in the MPR viewer segments. These lines define the area to be cut away. You can resize the crop region by clicking these orange lines in any of the image segments and drag them in or out, or you can rotate the crop region by dragging a corner.

When you have clicked a crop tool the **Lock Crop Region** icon appears in the lower right-hand corner of the active viewer segment. (The icons may look slightly different from this icon here, depending on which crop tool is currently active.)

Clicking this icon locks the crop region and allows you to move or rotate within the crop box or slab.

Tip

Show the bounding box in the 3D viewer segment before you select a cropping tool (see *3D viewer context menu options*). This will help you to identify the portions of the volume to be cut away.

Crop Box

Select this tool to cut away the outer parts of the volume. A smaller volume box in the center of the volume dataset remains. You can move, resize, or rotate this box by dragging or rotating it in any of the viewer segments.

Crop Corner

Select this tool to cut away a box from the corner of the volume.

Crop Slab

Select this tool to cut away portions of the volume so that only a slab remains (i.e. a section of the volume between any two parallel planes with oblique orientation.

Use the *Viewer controls* or the keyboard shortcut **T** in the 3D viewer segment to change the slab thickness or to toggle slab display on and off.

Crop Plane

Select this tool to cut away a corner of the volume along an oblique cutting plane.

Remove tools

These tools provide options for the automatic segmentation and removal of specific structures from 3D datasets. They also offer a subtoolbar for segmentation and cropping of freely definable volume sections. Freehand cropping can be performed in all datasets.

> **Caution**
>
> The automatic segmentation tools (remove table, remove leg bones, remove chest wall) support the physician by hiding structures that occlude important information in the images. However, the software cannot guarantee that the detected pixels correspond to the actual anatomical structures for each individual patient and scan. It is the responsibility of the user to check whether any relevant structure has been accidentally removed. In that case, simply click the respective tool icon to bring the removed structures back.

Freehand Crop

Click this icon to start freehand cropping. A context toolbar appears in the lower right-hand corner of the active viewer segment. Proceed as follows:

1. Select the viewer segment which shows the structure you want to crop particularly clearly.

2. Click and drag the mouse around the structure. When you release the mouse button the system closes the shape.

3. Select if you want to remove what lies inside your shape (**Remove Inside**) or what lies outside (**Remove Outside**) on the context toolbar.
The system now determines what to remove from the volume by extruding the drawn shape through all slices of the volume in the direction orthogonal to the current image plane. This portion is removed from the volume in the 3D viewer segment. Freehand cropping mode is also ended.

In order to work with the full volume dataset again:

1. Click the **Freehand Crop** tool a second time.

2. Click **Remove Reset** on the context toolbar in the lower right-hand corner of the active viewer segment.

3. Click **OK**.

Remove Table

If the table is shown in your images this tool offers a quick and easy way to remove this arti-fact in CT datasets.

Remove Leg Bones

Applies a lower extremities bone removal segmentation to a CT-Angio dataset, provided you have performed an automatic bone segmentation run during this or a previous session with this dataset. Bone segmentation with the *Bone tool card* is automatically stored by the system.

If no segmentation information exists for this dataset a message box informs you about this fact. Call the *Bone tool card* from this message box and perform bone segmentation now.

Remove Chest Wall

Click this icon to remove the chest wall/ribcage from a CT thorax dataset.

Fusion Registration tools

Visage 7 Client allows display of suitable datasets in so-called fusion display. Fusion display overlays datasets, for example, a CT and a PET series of the same study. Fusion display requires that datasets are registered, which means that they are aligned spatially.

When you load two datasets suitable for fusion display, Visage 7 Client displays a message that reminds you to check the correct alignment of the two datasets and confirm it manually. Unless you do so a warning triangle will be shown in the images throughout your entire session.

Close the message box and use the icons of the **Fusion Registration** toolbar to check, adjust, and confirm correct spatial alignment of your dataset pair.

Tip

Prior to aligning datasets manually you should window the two datasets in such a way that prominent structures are clearly visible (e.g. a bone). This will help you overlay the two corresponding images correctly.

Manual Registration

Click this icon to enter manual alignment mode. In this mode the two datasets are displayed overlaid. The primary dataset is shown in magenta, and the overlay dataset is shown in green in the active viewer. An outlined cross also appears in the MPR viewer segment.

Click the center of the cross, hold the mouse button down, and drag the green layer so that corresponding structures in the green and magenta layer are exactly overlaid. Release the mouse button when they are.

-Or-

Click one of the ends of the cross. The cursor changes shape and indicates rotation. Click and hold the mouse button down to rotate the green overlay layer.

Accept Registration

Click this icon after you have finished aligning your datasets manually.

Once you have clicked this icon, the warning triangle disappears from the image segments.

Align Centers

Click this icon to have Visage 7 Client align the centers of the bounding boxes of the two datasets.

Reset Registration

Click this icon to undo any manual or center alignment. The two datasets are now registered in the same way as they were right after loading.

Viewer Linking tools

Toggle Linking

Some protocols allow linked navigation in multiple viewers. When such a protocol is active you can use this icon to turn viewer linking on and off. When you navigate in a linked viewer the slice images in all linked viewer segments are updated accordingly.

Link Current Position I

When a side-by-side protocol is active you can link viewers on a certain landmark in the two datasets (e.g. a lesion, bone, or calcium segmentation).

Position the crosshairs on the landmark in both viewers and then click the **Toggle Linking** icon.

Reset Viewer Linking

Shows linked datasets in the same way as when you first loaded them.

Link Display Properties

Synchronizes window/level adaptation and display of thin or thick slices in all linked viewer segments.

Automatically Link Viewers

Click this icon to link viewers and the datasets displayed in these viewer segments automatically.

Edit Viewer Linking

Click this icon to link viewers and the datasets displayed in these viewer segments automatically.

CPR/Vessel tools

You use these tools to perform one of the following tasks:

- Definition and display of curved slices

  This implies that you define a curve through your volume and have Visage 7 Client apply curved reformatting, which shows a projection image of a curved extrusion plane defined by the vertices of your curve. This view helps tracking curved structures such as the spine.

  For curve definition you can either use the 3D viewer segment or MPR viewers or a combination of both. In MPR viewers you can scroll slices while adding points (vertices).

- Segmentation of vessels

  Semi-automatic vessel segmentation implies that you identify a vessel in the 3D viewer or any of the MPR viewer segments and define at least the start and end point for the vessel segmentation. Next you have the system segment the vessel automatically. Finally you can evaluate the vessel in your MPR viewers or in the lumen viewer.

  For a more detailed description of the procedures involved in vessel tracing and vessel analysis see also *Vessels and Centerlines tool card*.

Curved planar reconstruction

Curved View

CPR   Click this icon to show the curved slice viewer. The curved slice viewer is shown in a new viewer segment. As soon as you begin to click points along your curve a projection image is shown here.

Define/Edit Curve

Select this tool to begin curve definition. A context toolbar appears in the lower right-hand corner of your active viewer segment.

Now click the vertices of your curved slice in any of the viewer segments. The vertices and the curve will be shown in all viewer segments that display this data.

Use the **Show All Vertices** icon in the context toolbar to toggle display of all vertices that you have created so far, or only those in slices that are close to the currently displayed slice.

Use the **Undo** icon in the context toolbar of the active viewer segment to remove the last vertex. Or use the **OK** icon to finish curved slice definition.

Clear Points

Use this tool to delete a curve definition.

Toggle Centerline

Use this icon to show or hide your curve in the images in the MPR viewers and in the volume in the 3D viewer segment.

Vessel segmentation

Define/Edit Curve

Select this tool to begin curve definition. A context toolbar appears in the lower right-hand corner of your active viewer segment.

Click at least two points along your vessel to define the vessel segment you wish to review.

Curved View

Click this icon to turn display of the curved slice viewer on or off.

Lumen View

Click this icon to turn display of the lumen slice viewer on or off.

Cross-Section View

Click this icon to show a cross-section of your vessel in one of your MPR viewer segments.

Use the context menu in this MPR viewer segment to show the shutter as well.

Toggle Centerline

Use this icon to show or hide your curve in the images in the MPR viewers and in the volume in the 3D viewer segment.

Brain Perfusion tools

For brain perfusion studies, Visage 7 Client provides tools for performing perfusion analysis. The icons are sorted according to the workflow from left to right.

Display tMIP

Click this icon to show or hide the temporal MIP.

In a temporal MIP of a CT dataset, the brightness of each pixel in the image indicates the maximum pixel value in any of the time steps for this pixel. In MR datasets, **tMIP** shows the minimum pixel value. This helps to show contrast-filled vessels particularly clearly.

Define Artery

Next select **Define Artery** on the toolbar and click on the main artery of the brain in the temporal MIP image.

The point where you clicked is marked as a ROI and an uptake curve for this ROI is shown in the viewer. The update curve for the artery is displayed in red.

Define Vein

Next select **Define Vein** on the toolbar and click the main vein of the brain in the image.

The uptake curve of the vein has been added to the graph. The uptake curve for the vein is displayed in blue. If the graph is in your way, click it and drag it to where it does not hide important image information.

Calculate Perfusion

Click the **Calculate Perfusion** icon on the toolbar to show the following functional images in the result images viewer segments: mean transit time (MTT), time to Peak (TTP), cerebral blood flow (CBF), cerebral blood volume (CBV)

Define ROI

Select the original scan image, tMIP image, or any of the functional images (e.g. MTT) and click **Define ROI** on the toolbar to activate mirror mode and to define and evaluate regions of interest in this image.

A vertical line has appeared in the image segment. Click and drag the end points so that the line separates the left and right half of the brain.

Use the tools in the context toolbar in the lower right-hand corner of the image segment to define an elliptical ROI or a freehand ROI. As soon as you release the mouse button a mirror image of your ROI is shown in the other half of the brain. ROI statistics are shown in all four functional images.

The **Refine Contour** tool is active now. Correct the contour of the ROI you have drawn, do not correct the mirror ROI. Click anywhere in the image to show the "nudge" tool. This tool has the shape of a circle. The further away you click from the contour the larger the circle will be. The closer to the contour line you click the smaller will be. When you have clicked outside the contour you can use the nudge tool to push the contour line in and reduce the area defined by the contour. When you click inside the contour you can push the contour line out and increase its area.

Use the **Undo** icon on the context toolbar to undo contour editing step by step.

Click **OK** when you have finished refining contours and adding ROIs.

Mirror Mode

Use this icon to toggle mirror mode on an off.

Multiphase tools

Subtract baseline

Subtracts the baseline image from a time series.

See also *Additional tools for time series analysis*

Lesion tools

Lesion tool

With these tools and context toolbar you can mark lesions, segment lesions, and evaluate and compare lesions in a current and earlier study, for example.

To evaluate and compare lesions in a current and prior study proceed as follows:

1. Load the two studies onto the **View** window and show corresponding images side by side.

Tip: Linking the two viewers will help when you scroll while reviewing the datasets.

2. Click the lesion tool on the toolbar. A context toolbar is shown in the lower right-hand corner of the active viewer segment.

3. Use the **Segment Lesion** tool to segment and evaluate a lesion.

4. In the corresponding image of the other study either segment the lesion as well, or use the **Mark Lesion** tool to mark a spot if no lesion is visible in this dataset.

If you have segmented lesions in both images lesion statistics are shown, which include lesion growth information.

In order to grow or shrink a lesion segmentation:

Hold the **Shift** key down, click in the image and drag the mouse across the window. The lesion segmentation grows or shrinks and the lower threshold level for the segmentation is shown.

If a lesion cannot be segmented automatically (because of poor image quality, for example):

Use the **Measure Lesion** tool from the **Lesion** context toolbar to measure the diameter of a lesion in the images of one or both studies.

-Or-

Select **Measure Lesion (2 Diameters)** to measure both the horizontal and the vertical diameter of a lesion. (Note that your measurements must be perpendicular.)

In order to classify a lesion according to the RECIST standard:

Click a lesion to select it.

Drop down the list of standardized lesion labels next to the **Classify Lesion** icon to select one.

If you have marked several lesions in one or two corresponding datasets:

Use the **Next Lesion/Previous Lesion** tools in the context toolbar to scroll through all lesions marked in your dataset. (You can create snapshots for your report now, for example)

Labels tools
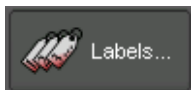
Labels... button

Opens a dialog to show labels of a study and create new or assign existing labels to the currently open so it can be quickly located, for example for conferences or a second opinion.

3. Click the **Labels...** button

4. In the dialog now opened, check one or more existing labels in the list box (you can filter this list by means of **show public** and/or **show private**)

- OR-

Create a new label by entering a name activating **Create Private** or **Create Public** to assign it to your own account or all users.

The selected label(s) or new label will be shown in a list. You can select an entry in this list and use the context menu to perform the following actions:

- make a private label public or vice versa

- delete a label

- assign it to a button on the labels toolbar.
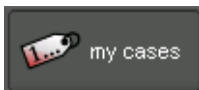
Label buttons

If a label was assigned to a button, it is shown on the Labels toolbar.

Miscellaneous tools

In this section you will find a description for additional tools and toolbars that are not contained in any of the standard toolbars by default. Most likely these tools will be available as separate toolbars which have been defined by the active protocol.

Magnifier

Use this tool to be able look at details in the displayed images more closely without having to zoom the entire image.

Select the tool and click in an image to enlarge a portion of that image just as if you were applying a magnifying glass.

Request original lossless data from server

If a red dot can be seen in the lower right corner of an image, this image has been loaded from the server in compressed form.

Press the **HD** button to force updating the image with lossless original data from the server.

Scroll Page by Page

Click this icon to use the wheel mouse for browsing images. In a 2D viewer segment that shows one image turning the mouse wheel will scroll one image at a time.

If the active viewer segment is a 2D viewer and several images are shown in the 2D viewer (tiled display mode) turning the mouse wheel will scroll one page up or down (i.e. replace all displayed images).

Study Navigator

Click this icon to open the **Prior Studies** dialog box with a list of any previous studies stored on the Visage server for this patient.

Study Information

Click this icon to open a dialog box with patient and study information.

You can edit the study comment text here but no other study information.

Tool cards

Tool cards may be arranged in one or several stacks, usually on the right-hand side of the window. Alternatively, tool cards can be displayed as floating windows.

Your currently active protocol defines how and how many of the available tool cards are shown right after you have loaded data onto the **View** window.

Showing a tool card

Click a tab in a stack of tool cards to call this card to the foreground.

-Or-

Select the tool card from the main menu (**Tools**).

The tool card will either be added to one of the stacks or be shown as a floating window.
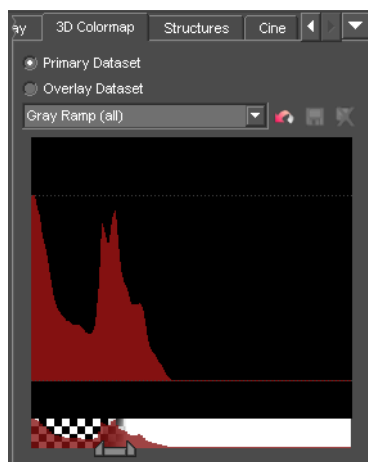
Tip

If you do not find the tool card you are looking for in the **Tools** menu then this tool card is deactivated in your current protocol. Select a different protocol in this case.

Tips for arranging tool cards

In order to show a tool card as a floating window, double-click its tab in one of the tool card stacks.

In order to attach a floating window to a stack of tool cards:

1. Click the arrow button that points down (upper right-hand corner of a stack of tool cards). A list of all available tool cards drops down.

2. Check more tools here to add their cards to your current stack.

A tool card can only be shown in one stack at a time.
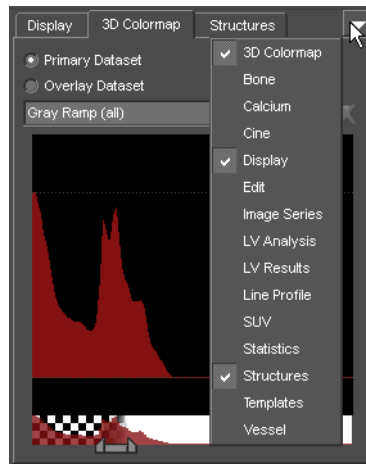
Some tool cards require more window space than others. You can therefore resize tool card stacks or the width of the entire tool card area.

1. Click the line that divides two stacks of tool cards, for example.

The mouse cursor changes shape.

2. Drag the line up or down to resize the tool card above and below.
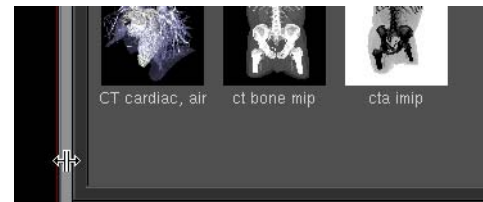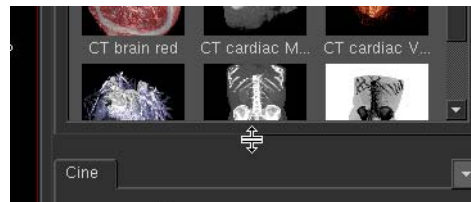
If the tool card area is temporarily in your way you can hide it:

Click the arrow button between the image viewer and tool card section.

-Or-

Uncheck **View > Show Tool Cards** in the main menu to do so.

Depending on the protocol, the tool card area may initially be hidden. In that case click the arrow icon at the border of the window.

-Or-

Select **View > Show Tool Cards** in the main menu to show the tool card area.

When tool cards are shown as floating windows they are usually displayed in a size that ensures they are not in your way while you are reviewing images. You can enlarge these windows, if you like.

Click the lower left or right-hand corner of the window and drag it out to show the tool card larger.

Visage 7 Client tool cards

Tool cards offer controls for changing image display settings and supporting the user with advanced image review and evaluation tasks. Some of these functions apply to all viewers, while others provide different tools depending on the currently active viewer type.

When the 2D viewer is your active viewer segment, most of the evaluation options on the tool cards are not available as they apply to volume datasets only.

Tip

If you cannot find one of the following tool cards in the drop-down list of tool cards or in the main menu, select a different protocol.

Templates tool card (3D viewer)

Templates offer a quick and easy way to optimize the 3D volume display in the 3D viewer segment for specific tasks.

A template defines volume rendering and display parameters for volume datasets of a particular modality or combination of modalities.

A template stores the following information:

- The modality of the primary and overlay dataset.

- A color map for the primary and overlay dataset

  See *3D Color Map tool card (3D viewer)*.

- Rendering and display settings for the volume display in the 3D viewer segment.

User-defined 3D templates

A number of predefined templates came with your system. Advanced users may choose to adjust these to their own requirements or define their own set of 3D templates. When saving a new or adapted template you decide whether to make it available for all users or save it under your own user account only.

Note

If you edit and save one of the *All users* templates on the Visage server you change this template permanently and for all Visage 7 Client users in your network. The factory-defined template version will be lost this way.
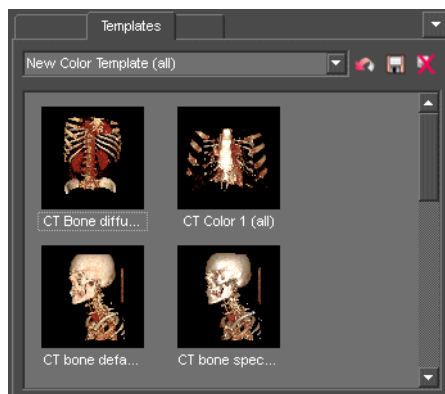
Template selection	Simply click a template thumbnail on the tool card.
	-Or-
	Drop down the list of suitable templates.
	The tool card lists only templates that were defined for the modality (or modalities) of the data currently loaded on the **View** window.
	After loading a template the volume display in the active 3D viewer is updated. You can work with this volume display now or change individual display parameters, if you wish.

 Click **Reset** to return to the original 3D volume and revoke your changes.

 Use these icons to maintain the list of templates available in your system.

Click the **Save** icon to save the 3D rendering and display settings currently applied to the 3D volume in your active 3D viewer segment.

A dialog box opens. Enter a template name here and decide whether the new template will be available for all users or for your user account only.

To remove this template from the list select a template thumbnail and click the **Delete** icon.

Display tool card

On the **Display** tool card you can adapt display settings for the images in the MPR viewers and the 3D volume in the 3D viewer. The **Display** tool card offers slightly different controls depending on the currently selected viewer segment (MPR viewer, 3D viewer, or 2D viewer), and whether fusion mode is currently active or not.

Turning fusion display on and off	If you have loaded multiple series or studies you can display the images of these series overlaid.

Click the **Primary Dataset** checkbox and the **Overlay Dataset** checkbox on the **Display** tool card and select datasets from the corresponding dropdown lists.

Fusion display is particularly suitable for studies from combined multi-modality scanners such as CT-PET and CT-SPECT, but you can also use this feature to overlay two CT series, for example.

Uncheck either the **Primary Dataset** checkbox or the **Overlay Dataset** checkbox to turn fusion display off again.

Display card in fusion mode (all viewers)

Primary Dataset	With this checkbox you turn display of the primary dataset on and off.
	Select the primary dataset from the drop-down menu (arrow button to the right).
Histogram and color map	Shows the histogram of the primary dataset.
	Use the slider right below the histogram to adjust the window settings for this dataset.
	-Or-
	Drop down a list of available color maps with the arrow button to the right of the histogram and select a suitable color map.
Overlay Dataset	With this checkbox you turn display of the second dataset on and off. This dataset will be overlaid over the primary dataset.
	Select the overlay dataset from the drop-down menu (arrow button to the right).
Histogram and color map	Shows the histogram of the overlay dataset.
	Use the slider to adjust the window settings for this dataset, or select a color map from the drop-down menu.
Fusion slider	This slider allows you to fade between the primary and the overlay datasets. If you move the slider all the way to the left, only the primary dataset will be visible. If you move it all the way to the right, only the overlay dataset will be visible.

Display card in non-fusion mode (MPR and 3D viewers)
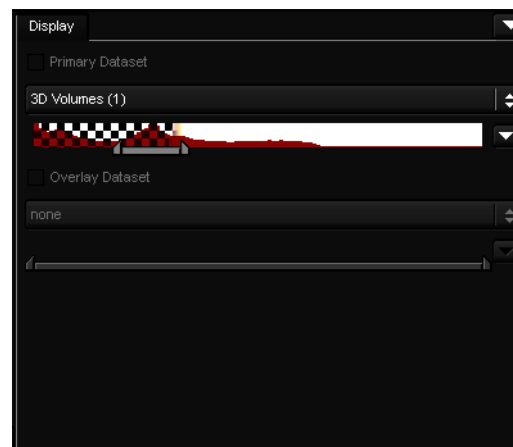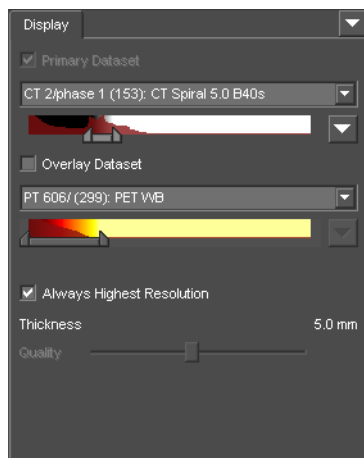
Dataset selection	Allows to select the dataset to be displayed.
Histogram and color map	Shows the histogram of the primary dataset. Use the slider right below the histogram to adjust the window settings for this dataset. -Or- Drop down a list of available color maps with the arrow button to the right of the histogram and select a suitable color map.
MPR/CPR/Lumen viewers	**Always Highest Resolution**: check this box to show full resolution images even during image manipulation (this may slow down program performance). Or uncheck this box to show a downsampled slice image during program interaction (e.g. for thick slices or during rotation). Use the **Quality** slider to decrease or increase image quality during program interaction: moving the slider to the right will increase image quality but may slow down system performance.

3D Color Map tool card (3D viewer)

The **3D Color Map** tool card allows you to select and edit the color map that is used for VRT rendering in the 3D viewer segment.

A color map assigns colors and transparencies to different tissue types as defined by their window values.

By selecting and adjusting a color map, you focus on structures and tissue types that are of particular interest to you. With a suitable color map, you can display these structures particularly clearly and hide structures and tissue types which would only distract you from the question at hand.

User-defined color maps

A number of predefined color maps came with your system. Advanced users may choose to adjust these to their own requirements or define their own set of 3D color

maps. When saving a new or adapted color map back to the Visage server you can decide whether to make it available for all users or save it under your own user account only.

Note

Some of the available color maps (e.g. *gray ramp* and *temperature*) can only be edited to a limited extent. Only the data windows of the tissue types of these color maps can be adjusted but not the color and transparency settings. Changes to these color maps cannot be saved either.
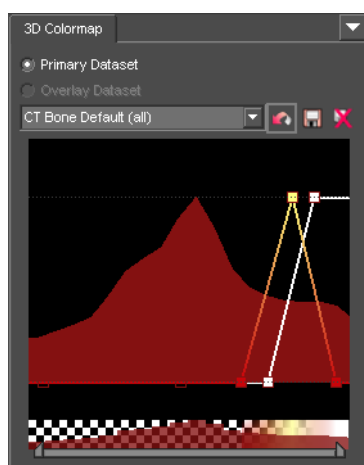
Primary Dataset/ Overlay Dataset	*Fusion mode only.* Select which of the two color maps you want to edit: the one that is used to display the primary dataset or the one that is assigned to the overlay dataset.
Color map selection	Click the arrow button next to the currently selected color map label to drop down a list of all color maps available in your system.
Color map editor	The color map editor shows the histogram (grayscale or HU values) of the selected dataset as a background image. The graphs that overlay the grayscale histogram represent the tissue types and their display definition with respect to color and transparency for VRT rendering. You can edit these graphs in order to change the color map: - You can change the data window for a tissue type. - You can select different colors for each graph. - You can change the transparency settings for a tissue type. - You can change the tissue type description. - You can add or delete tissue type graphs.

Click **Reset** to return to the original 3D color map and revoke your changes.

Use these icons to maintain the repertoire of color maps available in your system:

Click the **Save** icon to save your changes to a color map or create a new color map.

A dialog box opens. Enter a color map name here and decide whether the new color map will be available for all users or for your user account only.

To remove this template from the list select a color map and click the **Delete** icon.

Editing a color map   In order to move or resize the histogram:

1. Click in the black area above or below the grayscale histogram and hold the mouse button down.

   The mouse cursor changes shape (it turns into a double-arrow).

2. Drag the mouse to the right or left to move the histogram (and show areas to the right or left that were previously hidden).

   -Or-

   Drag the mouse cursor up or down to condense or expand the histogram.
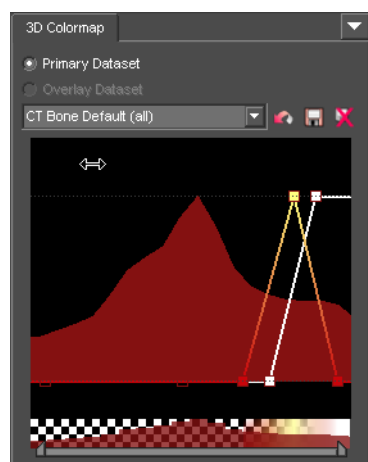
In order to add or delete a graph:

1. Right-click next to the graph to open a menu.

2. Select **New Tissue** to add a new graph.

   -Or-

   Select **Delete Tissue** to delete the selected graph.

   -Or-

   Select one of the listed tissue types for editing.

In order to edit a graph:

1. Click a graph to select it.

2. Drag the boxes to the left or right along the bottom line of the histogram to change the window center and width of this tissue type.

-Or-

Double-click the boxes along the bottom line or the apex (or apices) to change the color definition of the graph.

-Or-

Drag the boxes up or down to change transparency settings.

-Or-

Click in the tissue description text above the histogram and edit this text.
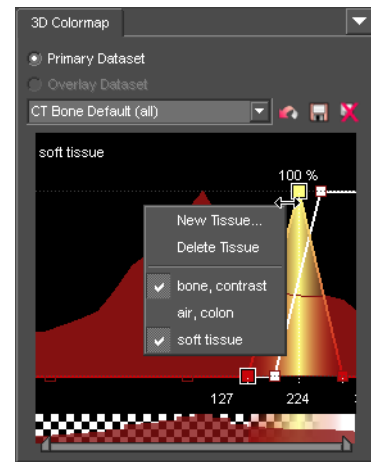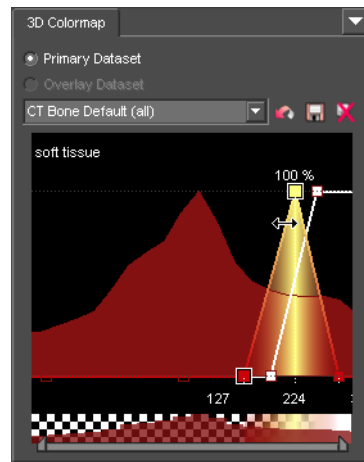
In order to rename a tissue type:

1. Click a tissue graph (control point or line) to select it.

The name of the selected tissue type is shown above the graph section.

2. Select this text in order to overwrite it.

Cine tool card

With the controls on the **Cine** tool card you can animate the display of the MPR and 3D viewers. Depending on the type of data that has been loaded and the selected viewer segment you can scroll through slice images in an image stack, play back a time series over time, rotate the volume in the 3D viewer segment, or move the crop plane through the volume (if the **Crop Plane** tool is currently turned on).

You can record these animations for presentation purposes, for example. You can save the resulting captured images as a new DICOM series (.dcm) in the local database or send them to another DICOM server in order to distribute the results of your work. Or you may save the images to the hard disk on your computer as MPEG movie (.mpg), JPEG (.jpg), PNG (.png), or DICOM (.dcm).

Cine tool card for MPR viewers (image stack or time series)
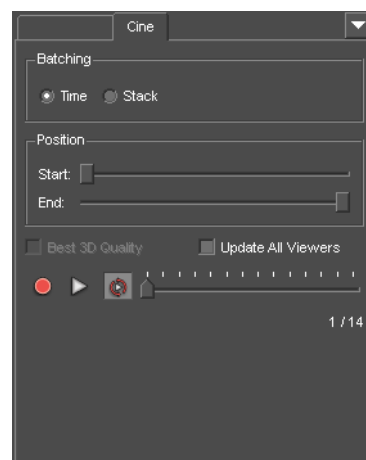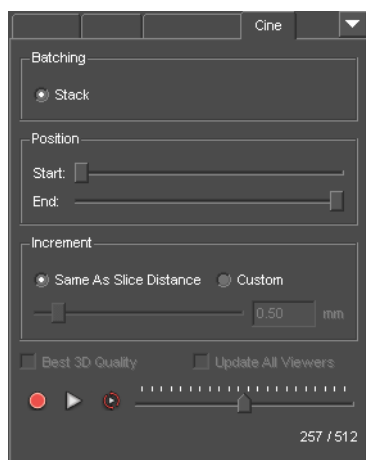
Batching	Select whether you want to scroll through the slice images (**Stack**) or whether you want to show a time series over the acquired time (**Time**).
Position	Select a **Start** position and **End** position slice for your movie.
Increment	Select an **Increment** for scrolling. This can either be the **Same as Slice Thickness** or any other value (**Custom**).
Best 3D Quality	Check this box for slow playback or recording in best 3D quality.
Update All Viewers	*Only active for time series.* With this checkbox you decide whether you want to apply cine mode to all viewers or whether you want to play the film in the selected viewer only.

 Click **Play** (or use the keyboard shortcut **C**) to play your film back once.

 Click **Pause** (or use the keyboard shortcut **C**) to halt the playback.

 Select **Loop** to play the film in an endless loop.

Click the **Record** icon to open the **Cine Options** dialog box.

Here you can choose whether you want to save your film as an MPEG movie (on your local computer), or as separate snapshot images (like in a slide show) or as a new DICOM series (on your local computer or on a connected DICOM server).

Cine tool card for the 3D viewer (image stack or time series)
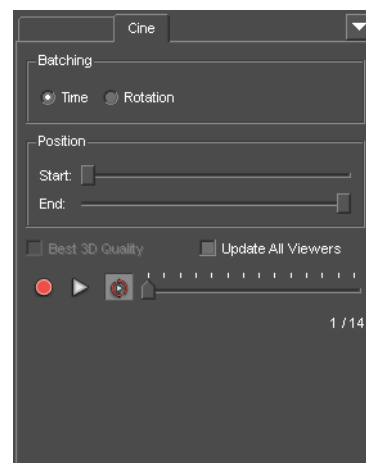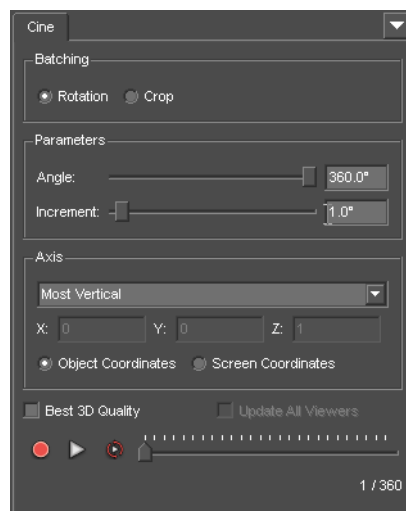
Batching	Select an animation mode here:
	Rotate - this rotates the entire volume.
	Crop - this has a crop plane move through the volume (only shown if the *Crop Plane* tool is currently turned on).
	Time - this plays the volume back over the time axis (only shown if the loaded dataset is a time series).
Parameters	Select the rotation **Angle** (360° is full rotation) and **Increment.**
Axis	Select a rotation axis and decide whether this axis refers to the patient coordinate system (**Object Coordinates**) or to **Window Coordinates**.
Position	Select a **Start** position and **End** position slice for your movie.
Best 3D Quality	Check this box for slow playback or recording in best 3D quality.
Update All Viewers	*Only active for time series.*
	With this checkbox you decide whether you want to apply cine mode to all viewers or whether you want to play the film in the selected viewer only.

Click **Play** (or use the keyboard shortcut **C**) to play your film back once.

Click **Pause** (or use the keyboard shortcut **C**) to halt the playback.

Select **Loop** to play the film in an endless loop.

Click the **Record** icon to open the **Cine Options** dialog box and save your film as an mpg file. Select recording settings here and choose whether to save the movie to your local computer or to a connected DICOM server.

Cine tool card for lumen viewer or CPR
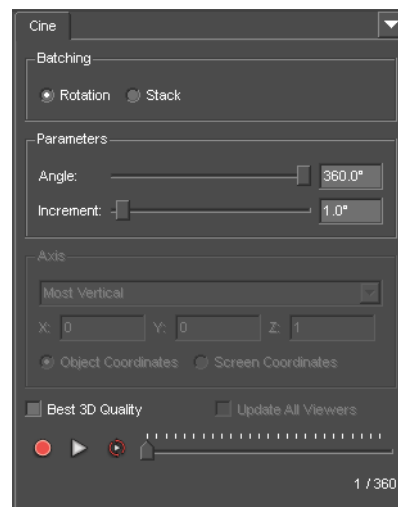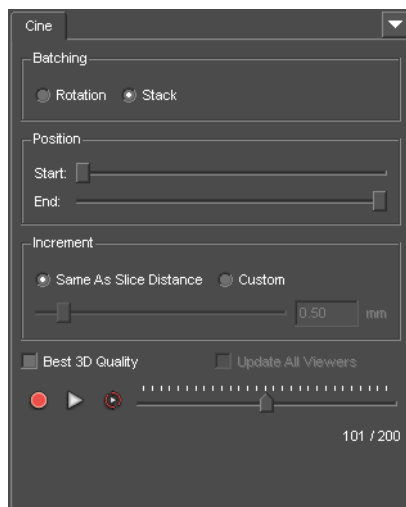
Batching	Select whether you want to scroll slice by slice (**Stack**) or whether you want to rotate around the segmented structure or vessel (**Rotation**).
Position and Increment	*If you have selected Stack mode:* Select a **Start** position and **End** position slice for your movie. Select an **Increment** for scrolling. This can either be the **Same as Slice Thickness** or any other value (**Custom**).
Parameters and Axis	*If you have selected Rotation:* Select the rotation **Angle** (360° is full rotation) and **Increment.** Select a rotation axis and decide whether this axis refers to the patient coordinate system or to window coordinates.
Best 3D Quality	Check this box for slow playback or recording in best 3D quality.
Update All Viewers	*Only active for time series.* With this checkbox you decide whether you want to apply cine mode to all viewers or whether you want to play the film in the selected viewer only.

Click **Play** (or use the keyboard shortcut **C**) to play your film back once.

Click **Pause** (or use the keyboard shortcut **C**) to halt the playback.

Select **Loop** to play the film in an endless loop.

Click the **Record** icon to open the **Cine Options** dialog box.

Here you can choose whether you want to save your film as an MPEG movie (on your local computer), or as separate snapshot images (like in a slide show) or as a new DICOM series (on your local computer or on a connected DICOM server).

Line Profile tool card

The **Line Profile** tool card shows the grayscale (or HU value) profile of the currently selected distance line in the image currently shown in the active viewer. If there is only one line in the image, that line is shown automatically.

If you have moved a distance line that was in your way no line profile can be shown. Move the distance line back to its original position to redisplay the line profile.
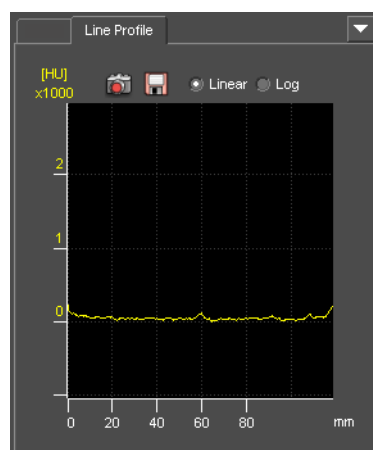
linear/log	Select linear or logarithmic scale.
x/y- axis	The x-axis shows the length of the line(s), the y-axis represents grayscale or HU values.
	In fusion mode (when a primary and an overlay image are active in the same viewer), two profiles are shown, one for each image. The colors of the lines correspond to the colors of the units shown on the two X axes.

Click this icon to create a snapshot of your line profile(s). The snapshot will be added to any snapshots of image data on the **Export** window, from where you can save it to hard disk.

Click this icon to save the data of your line profile onto your hard disk as a comma-separated list (*.csv file).

SUV tool card

PET images contain data that represent radionuclide activity in the patient's body. This data is usually indicated in units of Bq/ml. Visage 7 Client can convert these values in Standardized Uptake Values (SUV) based on the radionuclide activity and the patient's anatomy. Visage 7 Client algorithms for the following SUV standards:

• SUV based on body weight

• SUV based on lean body mass

• SUV based on body surface areas

On the **SUV** tool card you can select which value to use and check or correct the patient and study data required for SUV calculation.

Note

The values displayed on the tool card refer to the volume dataset currently shown in the active viewer. If you activate a viewer showing a different dataset, the values in the **SUV** tool card are updated.

Patient weight, height, sex	Check if this data has been entered correctly and add missing information if you want to calculate SUV for lean body mass or SUV for body surface area.
Radionuclide data	Check and, if necessary, add missing information on half-life, dose, injection and scan time start.
Reset to DICOM values	Use this button if you have changed data and want to reset it to the information stored in the source files.
Data Window	Adjust the SUV data window used for initial display in SUV-based protocols.
Unit radio buttons	Select the unit you want your system to use for displaying radionuclide activity in the patient's body. Choose between becquerel or Standardized Uptake Values, or select Counts for data acquired with Phillips scanners.

Make Default	Stores the default values for the initial data window as well as for the preferred SUV type in the global settings for this user.

Vessels and Centerlines tool card

This tool card helps you with vessel analysis as it allows you to trace one or several vessels in your dataset and name them, which will help you with reporting.

Vessel segmentation and analysis are performed in two steps:

• *Vessel tracing*

Visage 7 Client offers two alternatives or modes for vessel tracing: a semi-automatic mode and a manual mode.

In most cases you will use **semi-automatic vessel tracing** and click to select two (or more) points along a vessel and then have the system trace the vessel. If the system cannot trace and segment the vessel correctly you can reset tracing, return to curve definition, select more points and repeat automatic tracing. You will use the curve editing tools on the **Vessel** tool card or on the *CPR/Vessel tools* to do so. In semi-automatic mode the system will slightly readjust the points you clicked (for example, move a clicked point to the vessel center) and trace the path of the vessel automatically. Vertices you selected for semi-automatic vessel tracing are shown as green dots.

If semi-automatic vessel tracing fails to produce adequate results (for example, because of poor image quality) you can revert to **manual tracing mode**. Hold the **Shift** key down while you click vertices. Manually selected points are shown as blue dots and are placed exactly where you clicked. When you start vessel tracing the system connects all blue dots with straight lines and does not attempt to readjust points or trace vessel paths automatically.

Tip

Before you start vessel tracing rotate the volume in the 3D viewer and remove any obstructing structures so that you have a particularly clear view of the vessel or vessels in question.

• *Vessel analysis*

As a result of vessel tracing the system has identified your vessel in the dataset. The vessel is highlighted in the 3D viewer segment (surface shading).

You can now switch on lumen view, which helps you to locate areas of interest along your vessel. You can also show a cross-section of your vessel in one of the MPR viewer segments and use a shutter for easy navigation.

Vessel tracing

Click the vessel you are going to define.

Double-click the default text **Vessel1**, for example, and overwrite it with the name of the
vessel, if you want.

-Or-

Select **Insert New Vessel** from the context menu of the vessels list.

Click **Edit** to start curve definition. A context toolbar appears in the lower right-hand corner
of the active viewer segment.

For semi-automatic vessel tracing (green dots):

Click two points along your vessel to define the vessel segment you wish to review.

-Or-

For manual tracing mode (blue dots):

Hold the **Shift** key down while you click points along your vessel.

Click **Clear** if you have made a mistake and want to start again.
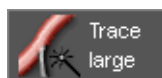
Click **Trace large** for large vessels (e.g. carotids or aortic vessels) or click **Trace small** for
small vessels (e.g. coronary arteries).
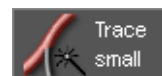
Visage 7 Client traces the vessel between the end points of your curve automatically now.

If automatic vessel tracing is unable to trace the vessel correctly, return to **Edit** mode to re-
fine your curve definition. Click to add more points, click an existing point to show images of
this point in MPR viewer segments, or **Shift** + click existing points to select them without up-
dating image display in the MPR viewer segments. Drag a selected point to move it

Vessel analysis   After you have had the system segment your vessel you can analyze it using the shutter view and the lumen view.

Click **Curved View** in the lower left-hand corner of the **Vessel** tool card to show a new viewer segment with a projection image of a curved plane defined by the vertices of your curve definition. Curved view allows you to rotate around a vessel, for example.

Click **Lumen View** to show a new viewer segment.

Lumen view helps you locate areas of interest along your vessel and navigate to these slices quickly. Simply drag one of the sliders to the slice you would like to review. This slice is now shown in the MPR viewers.

Use the lumen viewer context menu to show the distance between the sliders (**Segment Length**).

Dragging a slider also turns **Cross Section** view on, which replaces one MPR viewer segment. Use cross-section view to measure the vessel cross-section with the *Distance (D)* tool. Measurement results are shown in the lumen viewer next to the slider of the active cross-section.

Use the keyboard shortcut **E** to toggle cross-section display of the two sliders in lumen view.

Once you have measured the vessel cross-section in the images of the two slider positions, use the context menu in the lumen viewer to turn display of the percentage of the **Stenosis** on and off.

Shutter If the shutter is not already shown in the cross-section viewer, select it from the context menu. With shutter mode active:

You will navigate along the selected vessel when you browse slices in the segment with the shutter. (One of the sliders in lumen view will follow your movement).

You can rotate the vessel in **Lumen View** with the viewing angle handles in shutter view. Click and drag these handles to look at the vessel from a different angle.

You can resize the shutter. Hold the **Shift** key down, click one of the handles, and drag it in or out to shrink or enlarge the shutter.
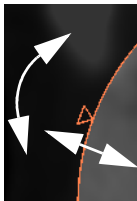
Bone tool card

The **Bone** tool card helps you remove bones from CT datasets of the entire body or of the legs.

Visage 7 Client can automatically delete and remove the pelvis and spine and the bones in the legs. Other bones cannot be segmented automatically.

Segmentation of bones with the tools of the **Bone** tool card is saved on the server automatically. No user interaction is required in this. The next time you load a dataset in which you performed bone removal in an earlier session you can also re-load your segmentation results. You can now apply them to the data again with the *Remove Leg Bones* icon of the **Remove** toolbar, or the option *Load Pre-Computed Segmentation* on the **Bone** tool card.

<table>
<tr><td style="background-color:yellow">Caution</td></tr>
</table>

The bone tool card supports the physician in finding bone structures in the image data.
However, the software cannot guarantee that the detected and displayed structures actually correspond to the bones of the pelvis, spine, and the bones of the legs. It is the responsibility of the user to check the plausibility and accuracy of the presented data.
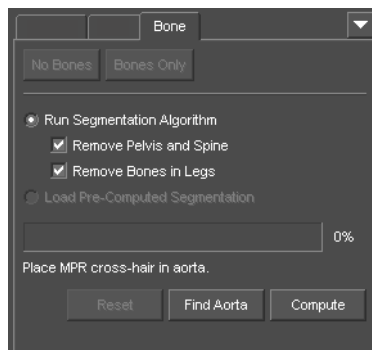
Segmentation al-gorithm	Select which bones you want the system to segment and remove: pelvis and spine, or the bones of the legs, or both.
Find Aorta	If you have selected pelvis and spine segmentation, the system expects you to locate the aorta. Either scroll to a slice that shows the aorta clearly and place the navigation cross-hair over the aorta. Or click this button to have the system find the aorta.
Compute	Click **Compute** to start the segmentation run.
No Bones / **Bones Only**	Use these buttons to toggle between hiding the bones in the 3D viewer, showing only bones, and showing the complete volume again.
Reset	Click the **Reset** button if you are not satisfied with the results of bone removal.
Load	Select **Load Pre-Computed Segmentation** and click **Load** to redisplay the results of a segmentation run you performed earlier or during a previous session.
	Selecting **Load Pre-Computed Segmentation** and clicking **Load** has the same effect as clicking the **Bone Removal** icon on the *Remove tools*.

Edit tool card

The **Edit** tool card allows you to segment structures, or to refine segmentation results created by semi-automatic Visage 7 Client segmentation tools, such as the bone removal tool.

Basic workflow

In order to segment a structure in your volume dataset, proceed as follows:

1. Select **Create New Object** in the context menu of the objects list in the lower half of the **Edit** tool card.

2. Point the mouse to the generic object name, select **Rename Object** from the context menu, and enter a descriptive object name.

3. Select the value range of the structure you are about to segment either by using the value range slider or by entering grayscale values or HU values (for CT data) in the min./max. boxes.

4. Click one of the selection tools above the value range slider (e.g. the **Connected Voxels in Value Range (3D)** tool).

   The system switches into a mode in which only voxels with grayscale values defined by the value range are shown in the 3D viewer segment. In MPR viewers tissue of this value range is highlighted blue.

5. Select voxels in the 3D viewer or one of the MPR viewer segments.

   Your selection is shown red.

6. Use the **Grow** or **Shrink** buttons to enlarge or reduce your selection, if necessary.

7. Click the plus sign (**+**) to the right of your object label in the objects list to add the selected structure to this object.

8. Use the context menu in the objects list section of the **Edit** tool card to control the display of segmented structures in MPR viewers (*Outlined in MPR*, *Filled in MPR*, or *Opaque in MPR*).

If your selection included more voxels than appropriate you can subtract them from an object.

1. Point the mouse to the object you have just created and select **Select this object** from the context menu.

2. Select the **Lasso** tool, hold the **Shift** key down and circle the section you want to remove from the selection.

-Or-

1. Click one of the selection tools above the value range slider.

   Only voxels with grayscale values defined by the value range are shown in the 3D viewer segment. In MPR viewers tissue of this value range is highlighted blue.

2. Identify the structure you want to remove.

3. Click the minus sign (**-**) to the left of your object label in the objects list to subtract the selected structure from this object.

Tip

Use the **Objects** control in the viewer controls of the 3D viewer and MPR viewers to adjust display options for any objects listed on the **Edit** tool card.

---

value range	Defines the value range for any voxels to be shown in the 3D viewer or highlighted in one of the MPR viewers after you have clicked one of the following selection tools.

With the **Connected Voxels in Value Range (3D)** tool you can click any point in the 3D viewer or an MPR viewer and the system will select all adjacent voxels of the same value range.

With the **Encircle Voxels in Value Range (3D)** tool you can draw a freehand shape around a structure either in the 3D viewer or any of the MPR viewers.

When you release the mouse button the system selects all adjacent voxels of the pre-defined value range within the freehand shape.
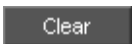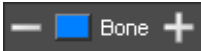
With the **Encircle Voxels in Value Range (2D)** tool you can select voxels in a single slice image only.

You use this tool if you need to work with extreme precision and proceed slice by slice.

With the **Define Contour in 3D** tool you proceed in the same way as when defining 3D structures with the *Structures tool card*: As soon as you click this tool a context toolbar is shown in the active MPR viewer segment. Select **Elliptical Contour** or **Freehand Contour** in this toolbar and draw a shape around the structure in this slice image. Scroll on to the next slice image that shows the structure in question particularly clearly and also define a contour. Click **OK** to finish contour definition.

Note that with the tool **Define Contour in 3D** you are expected to draw a shape as closely as possible around the boundary of your structure as it is shown in your slice images. This is because the **Contour** tool considers any voxels within your shape and not only those of the value range defined on the **Edit** tool card.

Grow	Click this button to increase your selection by one step. Use the **Grow 2x** button to increase your selection by two steps.
Shrink	Click this button to shrink your selection by one step. Use the **Shrink 2x** button to shrink your selection by two steps.
Clear	Click this icon to clear a selection.
— Bone +	Use the plus (**+**) sign in the objects list to add a selection (voxels highlighted red) to a object. -Or- Use the minus (**-**) sign in the objects list to remove a selection (voxels highlighted red) from a object.
🔒 🔓	Click these icons to lock or unlock objects. Locked objects are not affected when you add objects to a selection or remove objects from a selection (with the plus/+ or minus/- buttons).

Structures tool card

The **Structures** tool card provides tools for easy segmentation and analysis of structures such as tumors in CT or MR datasets.

Basic workflow

In order to segment a structure in your dataset you proceed as follows:

1. Decide whether you want to evaluate a 2D structure or a 3D structure and click the corresponding button on the **Structures** tool card.

2. Define its contour.

3. Refine this contour, if necessary.

4. For 3D structures scroll through your slice images and repeat contour definition in slices that show the structure in question.

   Visage 7 Client interpolates the contours and calculates the volume of the structure.

5. Click **Calculate Volume** on the structures tool card to have the system calculate the volume of your 3D structure.

6. Move on to the *Statistics tool card* to save the calculated volume and contour areas of your structures. You can send the data to the **Export** window from there, or export them to your hard disk as a comma-separated list file.

	Structure Name	Vol/Area	MPR	3D
■	2D ROI 1		☑	☐
■	3D ROI 2		☑	☐
	Contour 1	15.4 cm²		
	Contour 2	11.2 cm²		

New 2D | **New 3D** | **Delete**
Calculate volume | **Statistics…**
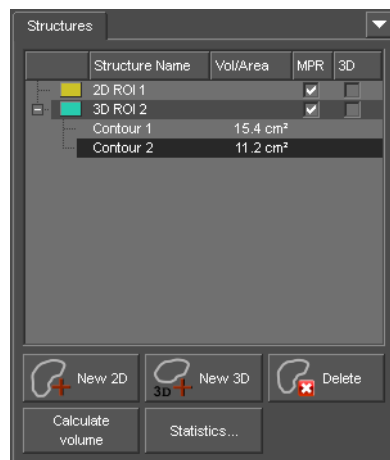
Structure Name	Lists all structures you have defined in your dataset and (for 3D structures) the contours that define them in a tree view.
	Structures and contours are numbered. Use **Rename Structure** and **Rename Contour** from the context menu in the structures list to give your structures and contours descriptive names.
Vol/Area	Shows the calculated volume for 3D ROIs and the area for 2D ROIs.
Color box	Visage 7 Client assigns each structure a color.
	Double-click the color box in the structures list to open the color selection dialog box. Select a different color, if required.
MPR	Check or uncheck these boxes for a structure to show or hide its contours in the MPR viewer segments.
3D	Check or uncheck these boxes for a structure to show or hide it in the 3D viewer segment.
New 2D	Click the **New 2D** button to create a new 2D structure. This requires drawing a contour in one slice image only.
	As soon as you have clicked this button a context toolbar is shown in the lower right-hand corner of the active viewer segment. This toolbar offers two alternatives to start contour definition: definition of an elliptical contour or definition of a freehand contour.
	Click in the image and draw your contour. When you have finished, the system switches into refine mode automatically. When you now click in the image a "nudge" tool is shown. This tool has the shape of a circle. The further away you click from the contour the larger the circle will be. The closer to the contour line you click the smaller it will be.
	When you have clicked outside the contour you can use the nudge tool to push the contour line in and reduce the area defined by the contour. When you click inside the contour you can push the contour line out and increase its area.
	Use the **Undo** icon on the context toolbar if necessary to undo contour editing step by step.
	Click **OK** when you have finished refining the contour.

Click the **New 3D** button to create a new 3D structure. This requires that you draw contours in more than one slice image and that you scroll through your image stack between contour definitions.

Use the tools in the contour toolbar in the lower right-hand corner of the active viewer segment as described above to refine your contours.

Click the **Delete** button to remove selected structures or contours from the list.
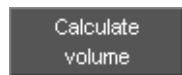
Click the **Calculate Volume** button to calculate the volume (mm³) of the selected 3D structure as well.

Click this button again each time you refine one of the contours that define a 3D structure.
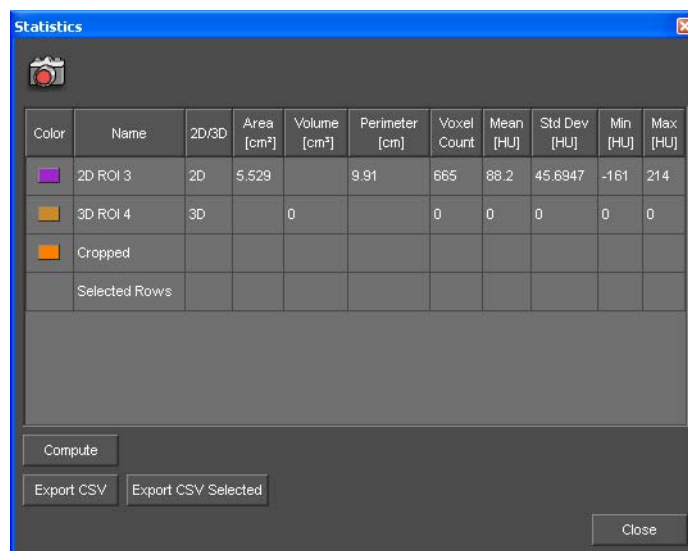
Click this button to open the **Statistics** tool card.

Statistics tool card

The **Statistics** tool card performs statistical analysis of all ROIs and structures that you defined in your primary dataset.

These are:

- A volume that you cropped using the *Freehand Crop* tools.

- The table, if you cropped it using the *Remove Table* tool.

- Bones that you segmented using the *Bone tool card*.

- Chest wall/ribcage, which you removed with the *Remove Chest Wall* tool.

- Vessels that you selected with the *Vessels and Centerlines tool card*.

- Structures that you defined on the *Structures tool card*.

- Objects which you defined on the *Edit tool card*.

- Lesions segmented volumetrically with **Segment Lesion** tool from the *Lesion tools*.

| Compute | Click **Compute** to have the system evaluate your ROIs and structures. |

In the columns **2D/3D** you can tell whether the evaluated ROIs are 2D (area) or 3D (volume) ROIs.

| Export CSV | If you want to continue evaluating the results of your ROI evaluation with another program (e.g. Excel), you can export them as a comma-separated list. |

Use the **Export CSV** button to export all your results or select **Export CSV Selected** to export the statistics of selected rows (i.e. selected ROIs or structures) only.

LV Analysis and LV Results tool cards

The **LV Analysis** tool card helps you with the analysis of the left ventricle in cardiac CT time series, which show the heart in various phases of one heart beat. This tool card guides you through an LV analysis step by step.

After you have completed the last step the **LV Results** tool card is displayed as a floating window. You can review your results now and export them to your report.

After you have just performed LV analysis the system cannot calculate the myocardial mass automatically. You need to identify the myocardium in your images manually first.

Caution

The LV tools support the physician in finding the left ventricle in the image data. However, the software cannot guarantee that the detected and displayed structures correspond to the left ventricle. It is the responsibility of the user to check the plausibility and accuracy of the presented data.

LV Analysis
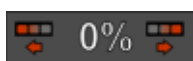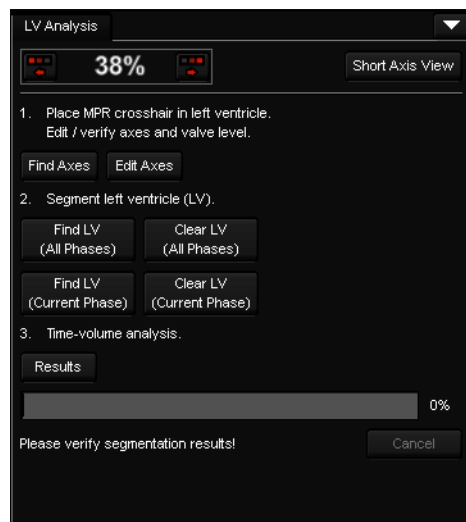
With the **Next Phase/Previous Phase** buttons you can page through the phase images one at a time

If you have moved or rotated your slice images, use the **Short Axis View** button to return to this view quickly. The button becomes active after you have finished the first step.

Step 1
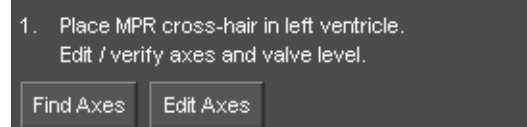
In this step you are expected to move the crosshair to the left ventricle in one of the MPR viewers. Click the **Find Axis** button when you are done. The system will now find the long and short axes of the left ventricle.

As a result the system will show the short axis view in one MPR viewer and long axis views in the other MPR viewers. In the long axis views the valve level is indicated as a pink line.

You are now expected to check the correct indication of the long axis and valve level in all phase images. Page through the phase images to do so.

If the axis or valve level are not indicated correctly in an image, you can adjust them: click the pink line in one of the slice images and drag it up or down.

Use the navigation crosshair in one of the slice images to move or rotate the axes: click close to the center to move the axis, or click far from the center to rotate it.

Decide whether to apply these adjustments to the currently displayed phase image alone or to all phase images (**Apply to all Phases** button in the context toolbar).

Click **Apply** in the context toolbar in the lower right-hand corner of the active viewer segment when you have finished your adjustments.

Step 2

Click one of the **Find LV** buttons to have the system segment the left ventricle either in **All Phases** or in the **Current Phase** your phase images. The segmentation results are indicated as shaded areas in the slice images. Page through the phase images once again to verify that segmentation yielded correct results in all phases if you chose this option.

If you do not agree with segmentation results in one or several images:

Click **Clear LV** and readjust the valve level and axes as described above.

Click the **Find LV** button again when you have finished your adjustments.

-Or-

Use the *Edit tool card* to edit the object LV manually. You can add or remove voxels in single or multiple time steps. Do not forget to unlock the LV object before you start editing.

Step 3
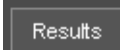
Click the **Calculate Perfusion** button when you are satisfied with the segmentation results in all images. The **LV Results** tool card is now shown.

LV Results

When displayed as a floating window the **LV Results** tool card consists of three segments: a summary section, a curve display section, and a section showing results in the AHA (American Heart Association) bull's eye view. When you display the **LV Results** card in one of the tool card stacks only one of these segments can be shown at a time.

Use the drop-down selection box in the lower left-hand corner of the tool card to select a different view of your LV analysis results.

Click the **Report** button to send your **LV Results** views to the **Export** window, where you can include them in your report.

Summary	Enter the heart rate of your patient here.
	The cardiac output value is updated automatically.
	Also adjust the system's selection of the end-diastolic (**ED**) and end-systolic (**ES**) phase with the sliders, if necessary.
Global Volume	Here you find a graph of the total LV volume over one heart cycle.
Bull's Eye View	View the results of the calculation of regional ejection fractions (%) in a bull's eye view.
	The segments in this bull's eye display correspond to the AHA classification.
	Move the mouse cursor over a segment to show the segment designation as a tool tip. Or right-click anywhere in the bull's eye view for a context menu that allows you to toggle between results view and segment ID view.
Regional Volume / Endocardial Distance	In this segment or tool card view you will find the stroke volume curves of the various LV regions.
	Initially the curves of all regions are shown. If you find this view hard to read, right-click anywhere in this section for a context menu that allows you to select and deselect region curves individually.
	Note that when you create a report only those curves that are currently shown will be included.
Wall Motion / Bull's Eye Motion	This segment or tool card view shows the accumulated wall motion in the bull's eye view.
	Move the cursor across this display to see region names as tool tips or right-click and toggle value and segment ID display.

Myocardial mass calculation

In order to calculate myocardial mass proceed as follows:
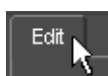
1. Open the **Edit** tool card.

2. Lock the object **Left Ventricle**.

3. Show a suitable phase image in one of the MPR viewers.

4. Select the **Define Contour in 3D** tool on the **Edit** tool card.

5. Draw a contour around the heart in the MPR viewer (prefereably in the short axis view). Adjust the contour, if necessary.

6. Scroll up or down a few images and repeat the last step for several images.

7. Add your selection to the object **Myocardium** by clicking the plus sign next to the object label on the **Edit** tool card.
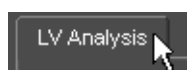
8. Return to the **LV Analysis** tool card.

	9. Click the **Calculate Perfusion** button again.
Results	

The system recalculates the LV analysis and adds the myocardial mass to the **LV Results**.

Calcium tool card

Visage 7 Client provides a tool card for identifying the extent of calcified plaque in coronary arteries for CT series.

Basic workflow   In order to perform calcium scoring you proceed as follows:

1. Select an MPR viewer that shows an axial slice (native thin-slice image).

2. Click the **Calcium Scoring** button on the **Calcium** tool card.

In your MPR viewers all areas with an intensity of more than 130 HU are high-lighted (blue).

3. You are now expected to scroll through the slices of your series and assign high-lighted (blue) areas to arteries.

Click the label button for an artery on the **Calcium** tool card. Then click on a blue highlighted area in your image or draw a lasso (click and drag). Scroll on to the next slice and repeat these steps.

The calcium score is updated every time you assign a new highlighted area to an artery.
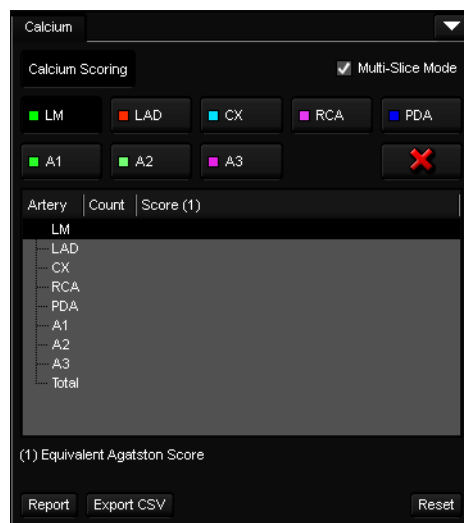
Calcium Scoring	Click this button to have the system identify areas with a HU value of 130 or more in your dataset.
	The button is active only if the active MPR viewer shows an axial native thin-slice image.
Multi-Slice Mode	Check this box if you want artery assignment to be applied to adjacent slices as well.

LM, LAD, CX, ...	Artery label buttons. Click a label button first and then assign it to a highlighted area in an image.
Results table	The results table lists the coronary arteries, the number of lesions found (according to Agatston Score) and the calcium **Score**, which is equivalent to the Agatston Score.
Report	Click the **Report** button to copy your results table onto the **Export** tab card, from where you can insert in into your report.
Export CSV	If you want to continue evaluating your results with another program (e.g. Excel) you can export them as a comma-separated list with the **Export CSV** button.
	With **Reset** you can delete any assignments you have so far made and start again.

Batching tools

Batching is a process in which special reformatting creates new image series.

The Batching tool is used to review/change the parameters of reformatting in a slice viewer or VRT before reformatting is started.

In addition, the properties associated with the batching workflow can be viewed and adapted if required.

Batching tool card

You can start batching on this tool card. In this process, regular linear or rotational stacks of images within a given dataset are defined. Three different methods of batching with different parameters are available:

- *Stacked Batching*
- *Horizontal Rotational Batching*
- *Vertical Rotational Batching*

Stacked Batching

	Allows to review/change the parameters of stacked batching. The parameters **Number of Images**, **Image Thickness**, **Overlap** and **Distance** are available.
	Clicking on the lock symbol before either **Number of Images**, **Image Thickness** or **Overlap** allows you to change this parameter by means of dragging the mouse within the viewer. Other parameters may be adapted automatically to keep the data consistent.

Properties...	Clicking this button opens the **Properties** dialog for stacked batching.
	The **Value** column will show possible changes you have already performed on the tool card.
	In the **Modified** column, a checked box shows that a value was changed, and in the **Defined in** column, the value will be set from **factory default** to **user profile**.
	You can click **Save in user profile** to save the changed parameters or reset to the factory defaults by clicking **Reset user profile...**
Save/Send	Initiates batching and a DICOM Send action. A dialog is opened where several properties (as in the Properties dialog) can be reviewed and changed.
	Select the receiving DICOM node under **Destination**.
	Under **Scout Images**, select the scout images you want to include, as well as **Show Measurements and Annotations** and **Show Orientation Cube**, if required.
	You can change the **Series Number** and **Series Description** or accept the defaults.
	Click **Make Default** to save your settings and click **Send** to send the stack to the selected DICOM nodes.
Export	Opens the **Export** dialog. Depending on your selection in the Properties dialog, the title bar of the dialog shows whether the stack will be exported as **Grayscale** (reformatting) or **RGB** (secondary capture).
	Select the file format under **Export as**. For a **Grayscale** export, only **DICOM Files** (dcm) can be selected. For an **RGB** export, **Image File** (**JPG** or **PNG**) or **Movie** (**MPG**) can be selected as well.
	You can enter the path for the export file under **Destination** and a file name or accept the given one. You can also **Browse** for a destination. The file type is automatically appended.
	The following **Options** are additionally available:
	• You can change the **Series Number** and **Series Description** for DICOM files.
	• You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** for image files.
	• You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** and additionally change the **Frame Rate** for movie files.
	Click **Export** to start batching and the export. A message is shown once it is finished.

Horizontal Rotational Batching

Allows to review/change the parameters of horizontal rotational batching. The parameters **Number of Images**, **Increment**, **Image Thickness**, **Overlap** and **Direction** (buttons for clockwise and anti-clockwise rotation) are available.

Clicking on the lock symbol before either **Number of Images**, **Increment** allows to change this parameter by means of dragging the mouse within the viewer. Other parameters may be adapted automatically to keep the data consistent.

Properties...	Clicking this button opens the **Properties** dialog for horizontal rotational batching.
	The **Value** column will show possible changes you have already performed on the tool card.
	In the **Modified** column, a checked box shows that a value was changed, and in the **Defined in** column, the value will be set from **factory default** to **user profile**.
	You can click **Save in user profile** to save the changed parameters or reset to the factory defaults by clicking **Reset user profile...**
Save/Send	Initiates batching and a DICOM Send action. A dialog is opened where several properties (as in the Properties dialog) can be reviewed and changed.
	Select the receiving DICOM node under **Destination**.
	Under **Scout Images**, select the scout images you want to include, as well as **Show Measurements and Annotations** and **Show Orientation Cube**, if required.
	You can change the **Series Number** and **Series Description** or accept the defaults.
	Click **Make Default** to save your settings and click **Send** to send the stack to the selected DICOM nodes.
Export	Opens the **Export** dialog. Depending on your selection in the Properties dialog, the title bar of the dialog shows whether the stack will be exported as **Grayscale** (reformatting) or **RGB** (secondary capture).
	Select the file format under **Export as**. For a **Grayscale** export, only **DICOM Files** (dcm) can be selected. For an **RGB** export, **Image File** (**JPG** or **PNG**) or **Movie** (**MPG**) can be selected as well.
	You can enter the path for the export file under **Destination** and a file name or accept the given one. You can also **Browse** for a destination. The file type is automatically appended.
	The following **Options** are additionally available:
	• You can change the **Series Number** and **Series Description** for DICOM files.
	• You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** for image files.
	• You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** and additionally change the **Frame Rate** for movie files.
	Click **Export** to start batching and the export. A message is shown once it is finished.

Vertical Rotational Batching

Allows you to review/change the parameters of vertical rotational batching. The parameters **Number of Images**, **Increment**, **Image Thickness**, **Overlap** and **Direction** (buttons for forwards and backwards rotation) are available.

Clicking on the lock symbol before either **Number of Images**, **Increment** allows to change this parameter by means of dragging the mouse within the viewer. Other parameters may be adapted automatically to keep the data consistent.

Properties...	Clicking this button opens the **Properties** dialog for horizontal rotational batching.
	The **Value** column will show possible changes you have already performed on the tool card.
	In the **Modified** column, a checked box shows that a value was changed, and in the **Defined in** column, the value will be set from **factory default** to **user profile**.
	You can click **Save in user profile** to save the changed parameters or reset to the factory defaults by clicking **Reset user profile...**
Save/Send	Initiates batching and a DICOM Send action. A dialog is opened where several properties (as in the Properties dialog) can be reviewed and changed.
	Select the receiving DICOM node under **Destination**.
	Under **Scout Images**, select the scout images you want to include, as well as **Show Measurements and Annotations** and **Show Orientation Cube**, if required.
	You can change the **Series Number** and **Series Description** or accept the defaults.
	Click **Make Default** to save your settings and click **Send** to send the stack to the selected DICOM nodes.
Export	Opens the **Export** dialog. Depending on your selection in the Properties dialog, the title bar of the dialog shows whether the stack will be exported as **Grayscale** or **RGB**.
	Select the file format under **Export as**. For a **Grayscale** export, only **DICOM Files** (dcm) can be selected. For an **RGB** export, **Image File** (**JPG** or **PNG**) or **Movie** (**MPG**) can be selected as well.
	You can enter the path for the export file under **Destination** and a file name or accept the given one. You can also **Browse** for a destination. The file type is automatically appended.
	The following **Options** are additionally available:

- You can change **Series Number** and **Series Description** for DICOM files.
- You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** for image files.
- You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** and additionally change the **Frame Rate** for movie files.

Click **Export** to start batching and the export. A message is shown once it is finished.

Batching toolbar

The batching toolbar is identical for the three different methods of batching:

- *Stacked Batching*
- *Horizontal Rotational Batching*
- *Vertical Rotational Batching*

RGB	**Toggle RGB/Grayscale**: Click this icon to switch the image generation mode between **Grayscale** (reformatting) or **RGB** (secondary capture).

Batch Send: Clicking this toolbar icon initiates batching and a DICOM Send action. A dialog is opened where several properties (as in the Properties dialog) can be reviewed and changed.

Select the receiving DICOM node under **Destination**.

Under **Scout Images**, select the scout images you want to include, as well as **Show Measurements and Annotations** and **Show Orientation Cube**, if required.

You can change the **Series Number** and **Series Description** or accept the defaults.

Click **Make Default** to save your settings and click **Send** to send the stack to the selected DICOM nodes.

Export: Opens the **Export** dialog. Depending on your selection in the Properties dialog, the title bar of the dialog shows whether the stack will be exported as **Grayscale** (reformatting) or **RGB** (secondary capture).

Select the file format under **Export as**. For a **Grayscale** export, only **DICOM Files** (dcm) can be selected. For an **RGB** export, **Image File** (**JPG** or **PNG**) or **Movie** (**MPG**) can be selected as well.

You can enter the path for the export file under **Destination** and a file name or accept the given one. You can also **Browse** for a destination. The file type is automatically appended.

The following **Options** are additionally available:

- You can change **Series Number** and **Series Description** for DICOM files.

- You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** for image files.

- You can select **Burn in Patient Information** and/or **Burn in Orientation Letters** and additionally change the **Frame Rate** for movie files.

Click **Export** to start batching and the export. A message is shown once it is finished.

Open Tool Card: Opens the Batching tool card, where you can select one of the three methods of batching and other options, as described under *Batching tool card*.

Cancel: Click this icon to cancel batching.

Additional tools for time series analysis

Visage 7 Client provides two additional functions specifically for time series analysis.

Time-density analysis for ROIs

Time-density analysis allows the observation of the density progression in a ROI over time in time-resolved 3D datasets.

The density progression is shown in a plot which displays the density graphs of one or several ROIs.

Basic workflow   **1.** Load a time-series.

2. Show an image from the baseline phase in an MPR viewer.

3. Draw a ROI.

See *Annotation and Measurement tools.*

4. Select **Time-Density Analysis** in the context menu.
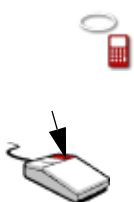
In order to add the time-analysis graph of a second ROI to an existing time-analysis plot:

5. Draw a second ROI.

6. Select **Add to Time-Density Analysis** in the context menu.

Subtraction for time series

Subtraction mode allows you to subtract the baseline phase from the other images of a time series. The resulting image shows only those structures where changes occurred over time now (e.g. the flow of contrast medium).

Basic workflow   **1.** Load a time-series.

By default the first image in a time series is the baseline phase (i.e. the image that will be subtracted from other images).

If you want to subtract another image:

2. Use the **Previous/Next Phase** icons on the *Dataset Navigation tools* to navigate to a different phase in the time series.

3. Select **Select as Baseline Phase** from the context menu to define this phase as the baseline phase.

4. Click the **Subtract zero phase** icon.

View window main menu

This section describes menus and commands that are available only if the **View** window is shown in the foreground.

Refer to *Getting Started* for a description of menu and commands available on all Visage 7 Client windows.

File	
Import DICOM Directory	Allows you to load a DICOM directory from hard disk, CD, or from an external drive.
	Return to the **Study Browser** after DICOM Directory import and load the data onto the **View** window from there.
Import DICOM Files	Allows you to load individual DICOM files from hard disk, CD, or from an external drive.
	Return to the **Study Browser** after DICOM file import and load the data onto the **View** window from there.
Save Protocol	See *Visage 7 Client configuration* (*Protocol configuration*).
Reload Protocol	See *Visage 7 Client configuration* (*Protocol configuration*).
New Session	Starts a new session.
Load Session	Loads a session that you have saved for this dataset.
Save Session	Saves changes to your current session.
Save Session As	Allows you to save your session under a new name.
Email Session Link	Allows you to send a session to a colleague as an attachment to an email.
	Do not forget to save recent changes to your session data before sending the link.
DICOM Job List	Shows a list of data retrieval and send jobs that are currently being processed. In the **DICOM Job List** dialog box you can cancel individual jobs or all jobs.
View DICOM Parameters	Allows you to show the DICOM information for the first image of each of the loaded datasets or slice images.
Preferences	Opens a submenu with configuration options.
	See *Visage 7 Client configuration* (*General preferences*).
View	

Viewer Proper-ties	See *Visage 7 Client configuration* (*Viewer Properties*).
Show Tool Cards	Shows or hides the tool cards section of the window.
Show Toolbars	Allows you to select which toolbars to show or hide.
Show in Viewer	Allows you to select which information will be shown as image text in the viewer segments.
Reset all Warn-ings	See *Visage 7 Client configuration* (*Reset All Warnings*).
Render Settings	See *Visage 7 Client configuration* (*Render Settings*).
Open Reports Viewer	Opens a window showing the latest report for the selected study.
Find Prior Stud-ies	Opens a window showing the currently loaded study as well as prior studies of this patient. Selecting one of more of these by means of the checkbox and clicking **Load** opens them on the View window.
UI Appearance	See *Visage 7 Client configuration* (*UI Appearance*).
Streaming Com-pression	See *Visage 7 Client configuration* (*Streaming Compression*).
Protocol	Allows you to select a protocol from the list.
	Default is the protocol that the system considers best-suited for the currently loaded vol-ume data.
	Under **Protocol > All > ...** you find a complete list of all protocols defined in your system sorted by monitor configuration.
Restored Ses-sion Protocol	Returns to the preset session protocol in case another protocol was used in the meantime.
Protocols list	The protocols that the system considers best-suited for the currently loaded data are listed first.
Configure Proto-cols	See *Visage 7 Client configuration* (*Prioritizing and disabling protocols*).
Tools	Allows you to select and show tool cards.

Export Window

You use the **Export** window to create reports for the study you have analyzed on the **View** window, or to save, send, or export snapshot images from here.

Basic workflow

When creating reports or saving or sending images you proceed in this order:

1. Load your study, series, or volume dataset onto the **View** window.

2. Show or create the relevant slice images.

3. Create snapshots of every image you wish to preserve.
   -Or-
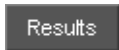
4. Send results of an LV analysis or a calcium score analysis to the **Export** window.

In order to create a report:

1. Select a template on the **Export** window (optional).

2. Drag snapshots onto your report page(s).

3. Add text.

4. Save and print your report.

In order to save or send snapshot images:

1. Select the snapshot images you wish to save or send on the **Export** window.

2. Click this button to save the images on your local computer or in your network.
   -Or-

   Click this button to save the images in your database or on another server in your DICOM network.

Overview of the user interface

Report editor toolbar

Snapshots

Report text

0%
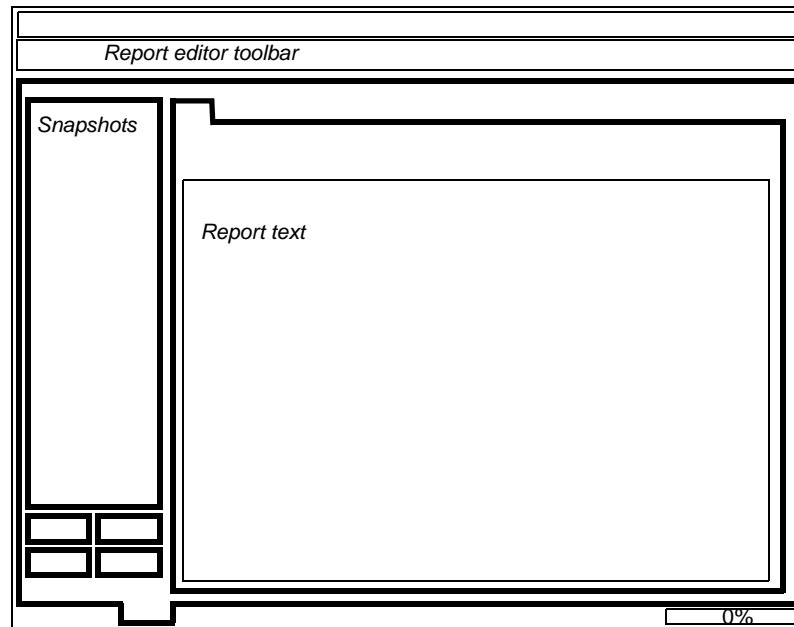
Snapshots

While analyzing images on the **View** window you create new slice images and add measurements and annotations. In order to document your results you can create snapshots of such images with the *Snapshot Active Viewer (S)* or *Snapshot All Viewers (Shift + S)* tools on the **View** window. Snapshots also include the results of LV or calcium scoring analyses sent to the **Export** window with the **Results** button on the corresponding tool card.

All snapshots you create during a Visage 7 Client session are collected in the **Snapshot** section of the **Export** window. From here you can save them, send them over the network or include them in your report.

1. Click a snapshot to select it.

-Or-

Hold the **Ctrl** key pressed while you click snapshots to select more than one image.

2. Click **Delete** to remove the selected snapshots from this window section.

-Or-
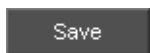
Click **Save** to export images onto your local computer or a network drive and folder in your network. Select DICOM, JPG, or PNG as a file format.

Use the **Send** button to save selected snapshot images in your local database or DICOM network.

A dialog box opens when you click this button. Select **Local** here to save the selected snapshot images in the database. The images will be added to a study as a new series.

-Or-

Select one of the configured remote DICOM nodes to send the selected images in your DICOM network.

> **Note**
>
> If you select multiple images and save them as DICOM or send them to a DICOM server, a new DICOM series will be created assigned to the original study.
> If you select images from multiple different studies, one new DICOM series will be created for each of the studies, containing only the images belonging to that study.

-Or-

Select **Web Client** to show the selected images in a Visage Web Client image viewer. The button only becomes active once snapshots have been sent to the local database

Report editor toolbar

The toolbar section comprises several toolbar sections:

File

With the icons of the **File** toolbar (or the commands of the **File** menu) you can:

- Create a new report.

- Print your report or show a print preview.

- Create snapshots of your report pages (one per page). The generated report snapshots will be shown on the thumbnails section on the left side, so that you can export the report pages as images, save them in the Visage image database, or send them to any DICOM partner.

- Create a PDF version of your report.

- Create a Word document.

- Send the report to the RIS (depending on configuration/RIS integration).

- Close the report you are currently working on.

Templates

When you create a new report you can select one of the report templates stored in your system.

If you have made changes to your template that you would like to reuse in future reports, click the **Save** icon next to the template drop-down list. You can either overwrite an existing template or create a new one now.

Format Actions

Use these two toolbars (or the commands of the **Format** menu) to perform one of the following text formatting operations:

- Format selected characters or words as bold text or in italics, or underline them.

- Change the color of selected text.

- Re-align text (left, center, right, or justified).

- Apply predefined paragraph styles.

- Select a different type font or font size for selected text.

Edit Actions

With the icons of the **Edit Actions** toolbar (or the commands of the **Edit** menu) you can:

- Undo the last editing action (or redo the last action you undid).
- Cut or copy selected text to the clipboard, or paste text from the clipboard.
- Search for text or search and replace text.

Report text

In the report text section of your report editor you can type text, insert snapshot images, or insert placeholders for patient and study information.

Inserting snapshots   Select one or several snapshots in the **Snapshot** section of the **Export** window and drag them into the report text section to include these images in your report.

Placeholders   Use the **Edit > Insert Placeholder > ...** menu to select and insert a placeholder into your report text. Placeholders are populated with patient and study information as soon as you insert snapshots into your report.

Placeholders are particularly useful when you create report templates.

Diagnostic Report

Patient Information	Study
Patient Name: <PATIENTNAME>	Study Date: <STUDYDATE>
Patient Gender: <GENDER>	Study ID: <STUDYID>
Date of Birth: <DATEOFBIRTH>	Report Date: <REPORTDATE>
Patient ID: <PATIENTID>	Exam Type: <EXAMTYPE>
Referring Physician: <MDREFERRING>	Accession Number: <ACCESSNUMBER>
Report Creator: <USERNAME>	

Tip

If you try to combine snapshots from several studies in one report, a message will prompt you to confirm this. The message will also remind you to check study-specific information and ensure that placeholders have been populated correctly.

Quality Assurance

You can use **Quality Assurance** (QA) to manually fix incorrect patient, study and series data, to re-assign images to the correct patient, study or series, to merge patients or delete patient entries, and to match studies with orders sent by a RIS system.

By default, all studies will be shown **Performed Procedures** list. Filter for studies with QA status "SCHEDULED", indicating that automatic data consolidation did not produce satisfactory results, to view studies which need to be QA processed.

Orders from the RIS can be displayed in the **Scheduled Procedures** list.

Dedicated QA user rights are required to perform QA activities.

Overview of the user interface

Quality Assurance window menu
Presets bar

Query section	Performed Procedures list (studies)
	Scheduled Procedures list (orders)

Query section

Study/Order   Queries can be applied either to the studies list (performed procedures) or to the orders list (scheduled procedures), with slightly different filter criteria.

Modality search   The query section allows you to search a database for studies performed on one or several modalities. E.g. check CT, MR, and DX modalities in the query section to show all items relating to any of these modalities. You can toggle the modality search on and off by means of the checkbox.

Filter criteria   All other entry boxes in the query section are filter criteria. This means, the more criteria you define, the shorter the hit list will be. E.g. enter A for patient name to show all patients whose name starts with an A. Or enter A for patient name and select today for study date to show only those patients whose name starts with an A **and** who were examined today.

Wildcard search   If you do not remember a name or number you are looking for, you can use wildcards in your search. E.g. type **Mil** in the patient name box to find **Mil**ler, **Mil**ford, **Mil**tner, or ***mil** to find all the above and also Ha**mil**ton, or **AB??34** in the patient ID box to find **AB1234**, **AB0034**, and **AB11345678**.

Even if you use wildcards, you should always specify your search criteria as precisely as possible. Rather general queries may yield a very long hit list, which would require extensive scrolling.

Filter and search criteria

First toggle between the **Study** and **Order** tabs, depending on the search you want to perform. The Query section will appear slightly different for each of them.

Searching on the **Study** tab produces results in the *Performed Procedures list*, whereas the **Order** tab produces results in the *Scheduled Procedures list*.

Patient	Allows you to search for a patient's name and ID.
Date	Allows you to search for patient and study data based on a date or date range. You can toggle the date search on and off by means of the checkbox.

Type - select whether you want to search by

- **Study Date**, **Date of Birth** or **Insertion Date** (i.e. the date when the data was transferred to the server) on the **Study** tab
  - OR -

- **Date of Birth** or **Modification Date** (i.e. the date when the order was modified) on the **Order** tab

From *date* **To** *date* - specifies the search period. Click in a date box with the cursor and enter a date in the format YYYY-MMM-DD (e.g. 2006-MAY-23). Or click the icon button to the right of the date entry box to open a calendar and select a start and end date from here.

Click one of these buttons to select a default search period:

Today - selects the current day as search period.

Yesterday - selects the previous day as search period.

1 Week - selects the last seven days as search period.

2 Weeks - selects the last 14 days as search period.

Modality	Allows you to search for patient and study data by modality. You can toggle the modality search on and off by means of the checkbox.

Choose one of the following options:

1. Check the boxes of all those modalities whose studies you are looking for (**CT** - computed tomography, **DS** - digital subtraction angiography, **DX** - digital radiography, **MR** - magnetic resonance tomography, **NM** - nuclear medicine, **PT** - positron emission tomography (PET), **US** - ultrasound, **SC** - "secondary capture" images)

2. Enter any modality abbreviations in the **Others** box (e.g. "CT"). Multiple modalities are separated by a space (e.g. "CT PT MR").

Fields	Here you can specify further filter criteria. These are specific either for a **Study** or **Order** search.

Drop down a list of available criteria with the arrow icon to the right of a field box. Then specify your search string in the input box below the selected criterion.

In addition, you can

- click **Study States** and then select one or several study states in the dialog to be included in your search on the **Study** tab. Clicking the **Clear** button resets this selection to include all study states.

  - OR -

- select an order status from the **Status** drop down list on the **Order** tab.

Starting and resetting a search
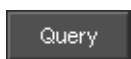
Query	Click this button to start your query of the local database or the DICOM node whose tab card is currently shown in the study/series list area.
	Click this button to remove all search criteria from the query boxes, then start defining a new search.

Presets bar

The Presets bar contains the button **New Preset**, which opens a dialog to define the current settings, for example a specific query, as a preset for the currently active user. This preset will then be shown as a button on the Presets bar.

You can

- enter a name for the preset.
- check **auto query** to automatically start a query when the preset button is clicked.
- check **Default** to define this preset as default for your user account, loading its parameters when the Quality Assurance view is opened.

Context menu of the preset buttons

Clicking a preset button with the right mouse button opens this context menu.

Properties	Allows you to change the preset's name and to have the preset perform an **auto query** or set it as **Default**.
Default	Checking this menu option defines this preset as default, loading its parameters when the Quality Assurance view is opened.
Update preset with current settings	Updates the preset with the settings currently active in Quality Assurance.
Delete preset	Deletes the preset button after a query is confirmed.

Performed Procedures list

The initial contents of the Performed Procedures List depend on your default query preset. Typically, the studies with QA status "SCHEDULED" will be shown, since these are most likely to be in need of manual correction.

Information in the Performed Procedures list

The Performed Procedures list is arranged in a hierarchical tree view. Use the **+/-** icons in front of the entries to expand or collapse the list.

Patient Name	Name of the patient.
Patient ID	Patient's identification number.
Birth Date	Patient's date of birth.
Sex	Patient's sex (M/F/O)
QA Status	QA status of the study. Possible values are NOT SCHEDULED, SCHEDULED, COMPLETED and DISCONTINUED.
Accession Number	Job number of the patient in the HIS/RIS (hospital or radiology information system).
Study ID	ID of the study.
Modality	Modality or modalities used to examine the patient.
Body part	Body part examined in this series.

Images	Number of images in a series or volume dataset (on the study level no image number is shown).
Description	Study or series description.
Comments	Study comment from the DICOM images.
Date/Time	Date and time when the study or series was performed in the format YYYY-MMM-DD and HH:MM:SS (24 hour clock).
Performing Physician	Performing Physician entered for this study or series.

Menu and Icons of the Performed Procedures list

These commands can be found in the **Edit** menu of the menu bar as well as in the context menu. The items of the Edit menu can also be displayed as an own menu bar.

The functions can also be called up via icons in the toolbar.

Move	Moves one or more images, series or studies to other existing series, studies or patients. At least two items must be selected. Items can only be moved to items on a higher hierarchical level, like this:
	• Images can be moved to series, studies or patients. If they are moved to a patient, a new study and series are created, if they are moved to a study, a new series is created.
	• Series can be moved to studies or patients. If they are moved to a patient, a new study is created.
	• Studies can only be moved to patients.
	After selecting two items and clicking on **Move**, a safety query is displayed, so that you can check your selection before confirming it.
Split	Splits the selected study/studies or series and creates a new data record to receive your selection. You will be prompted to enter data on patient or study level for the new data record.
Move to New Patient	Move one or more selected series to a new patient. You will be prompted to enter patient information for the new patient that will automatically be created to receive the selected series. Click **Force Update** if you want to update the DICOM files even if no changes to the database are made.
Merge Patients	Merges two selected patient data records into one. You will be prompted to select the target data record to which the other one should be assigned, which is deleted after merging.

Edit   Lets you change a data record on patient, study or series level, depending on your selection. Click **Force Update** if you want to update the DICOM files even if no changes to the database are made.

Delete   Deletes one or more selected images, series, studies or patient entries after you confirm a safety query. Check **Delete from Archive** in the safety query if required.

Assign Order to Study   Assigns a study selected in the **Performed Procedures** list to an order selected in the **Scheduled Procedures** list. You are prompted to confirm the assignment.

Scheduled Procedures list

The Scheduled Procedures list contains the scheduled procedure steps sent by the RIS. Some of them may have to be manually matched to studies.

Information in the Scheduled Procedures list

The individual columns contain information on patient, visit and order level provided by the RIS, with the exception of the **Assigned** column, where you can see whether an order has been assigned to a study or not.

Menu of the Scheduled Procedures list

The only command available for the Scheduled Procedures list can be found on the menu bar as well as in the context menu.

Assign Order to Study	Assigns a study selected in the **Performed Procedures** list to an order selected in the **Scheduled Procedures** list. You are only prompted to confirm the assignment.

Visage 7 Client configuration

Users can adapt program functions and the appearance of the Visage 7 Client user interface to a certain degree. Some of these configuration options are available to all users while others can only be accessed by users with appropriate user rights. Users with the right to access these preferences can also save their settings. Again depending on their user privilege settings these changes will be effective for their own user account only or on a system-wide basis.

> **Tip**
>
> If you cannot access some of the commands and dialog boxes described in this section, this indicates that your user account has not been assigned the appropriate user rights.
> Talk to your system administrator about the organization of user privileges in your institution.

All configuration options are accessible from the main menu, some configuration options are available on all windows, while others can be acessed from the **View** or **Study Browser** window only.

General preferences

Select **File > Preferences** from the **Study Browser** or **View** window to drop down a submenu with the folllowing configuration options.

- *Window/Level Presets*
- *Properties*
- *Tool Palette*
- *Properties*
- *Monitor Configuration*

In order to be able to access these configuration dialogs you need to be assigned to a user level with the right to manage properties on a user or system level. Monitor configuration is available to all users irrespectively of their user level.

Monitor Configuration

If you are working with more than one monitor, this configuration dialog box allows you to define which Visage 7 Client window will be shown on which monitor.
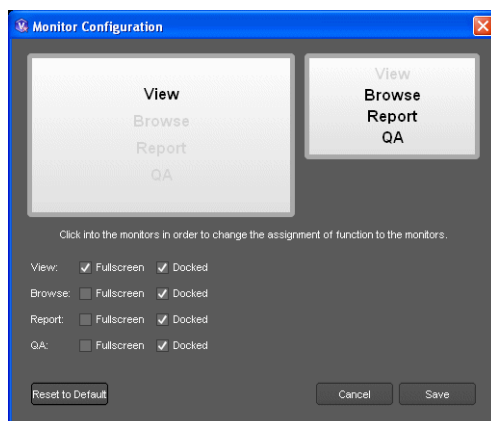
Window/Level Presets

In this dialog box you can define **Window/Level Presets** for image types. Either enter the relevant parameters or copy settings from the currently active viewer.
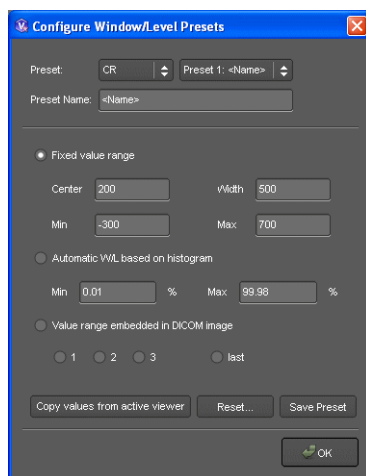
Window/Level Presets can be called from a drop-down menu in the viewer controls below each viewer segment and via the available shortcuts (1, 2, 3, 4,...).
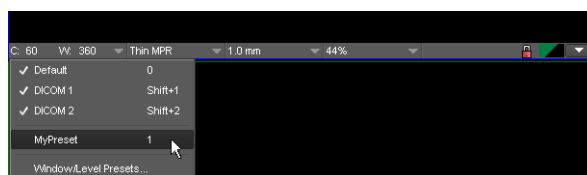
Keyboard Shortcuts

Visage 7 Client comes with a set of predefined keyboard shortcuts for frequently used functions and tasks. You can display this list by selecting **keyboard shortcuts** from the **Help** menu.

In the **Configure keyboard shortcuts** dialog box you can adapt the assignment of keyboard shortcuts to your own preferences.

Select a tool in the **Available Tools** list to the left and drag it onto a key or key combination to the right to assign or reassign a tool to a keyboard shortcut or key combination.

Click with the right mouse button on an assigned tool and select **Remove** from the context menu to remove this tool from the keyboard shortcut or key combination.
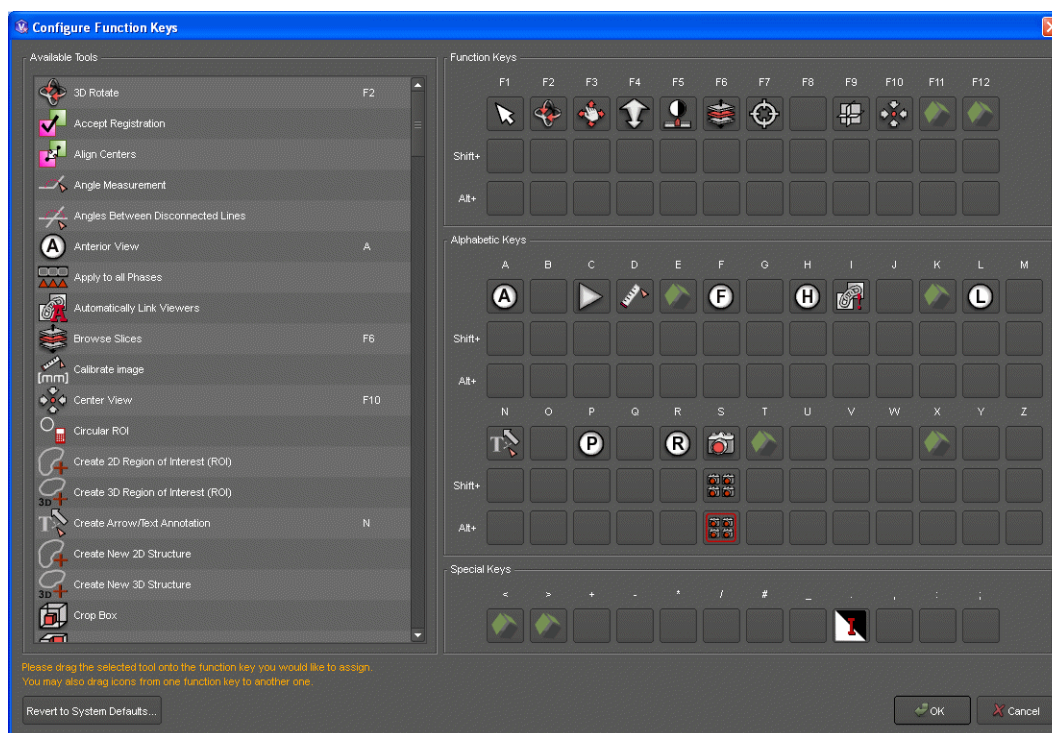
Tool Palette

In the **Configure Tool Palette** dialog box you can assemble a toolbar with frequently used tools. By saving this collection of tools for your own user account you create a personal toolbar or palette.

Click with the right mouse button on an assigned tool and select **Remove** from the context menu to remove this tool from the tool palette.
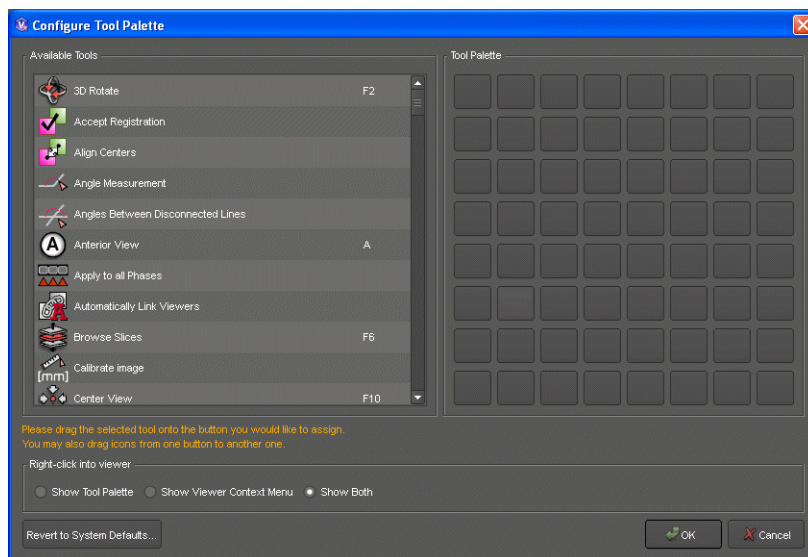
You can choose whether a right-click into the viewer will show only the tool palette, only the context menu entries, or both.

Properties

This dialog box shows the default settings for the majority of program functions and features. The **Properties** dialog box also indicates whether a setting is a factory default or a system or user level configuration setting. You can adapt configuration details here. Moreover, with the appropriate user privileges, you can change the assignment of settings to the user or system level.
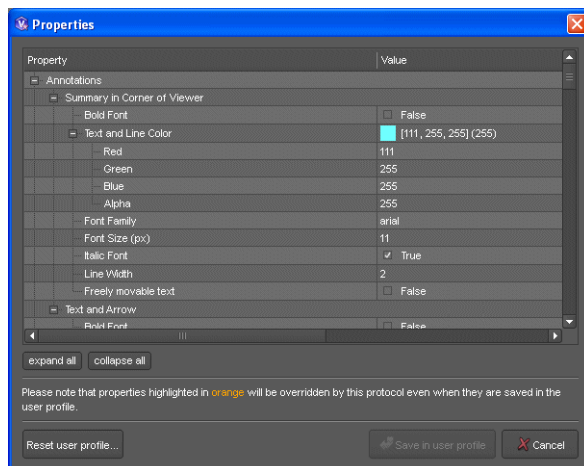
Display settings

Drop down the View menu of the **Study Browser** or **View** window for a number of configuration options that affect **View** window or image display aspects.

- *Viewer Properties*

- *Reset All Warnings*

- *Render Settings*

- *UI Appearance*

- *Streaming Compression*

Viewer Properties

This dialog box shows allows you to define display settings for the **View** window user interface. The **Viewer Properties** dialog box also indicates whether a setting is a factory default or a system or user level configuration setting. With appropriate user privileges you can change the assignment of configuration settings to user or system level here.
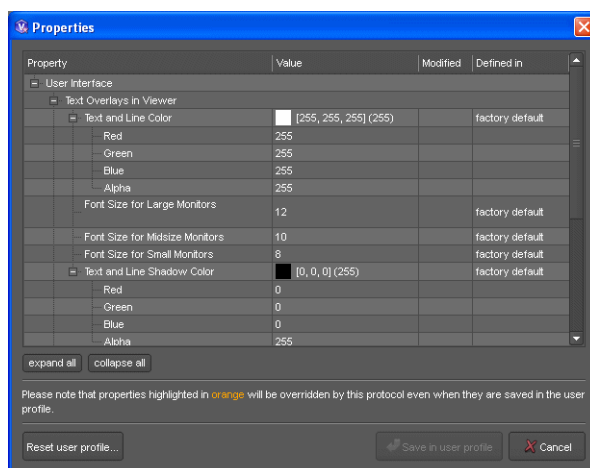
Tip

The **Viewer Properties** dialog box shows a subset of the user interface configuration options of *Properties* dialog for a better overview.

Reset All Warnings

If you had selected *Do not show again ...* for any warning that appeared since you called up Visage 7 Client, selecting **View > Reset All Warnings** will make sure that a warnings are shown again from now on.

Render Settings

This dialog box allows you to define render settings for the server and the local rendering subsystem.

Check the **Auto** checkbox for **Local Rendering** and **Rendering Subsystem** to have the system identify and select the option best suited for your system configuration.
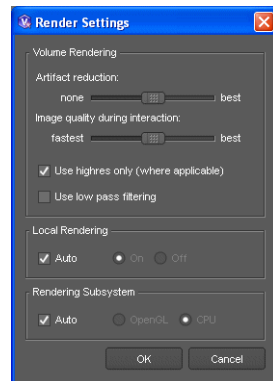
Caution

Only use **Local Rendering** set to **ON** and **Rendering Subsystem** set to **Open GL** manually if you are certain that this mode is supported properly by the graphics card in your client computer.
Validate correct image display by loading and displaying test images.

UI Appearance

View > UI Appearance opens a submenu which allows you to choose between different color schemes for the user interface: bright, medium, and dark. This allows you to adapt the user interface to the ambient light conditions of your workplace.

Streaming Compression

Selecting **View > Streaming Compression** allows you to select a compression level for image transfer from the server to the client computer.

Select a compression level depending on the network you are working in and on the image quality you require (the system will remember your selection):

- **Auto** - selects a compression level that has been optimized for the current network bandwidth and latency characteristics.

- **Lossless Only** - transfers only losslessly compressed data with full image quality. Select this option for fast networks, for example, in local area networks (LANs). Your server needs to be configured to support this function.

- **Medium** - applies a medium compression level. Select this option, for example in a slow LAN or a wide area network (WAN).

- **Strong** - applies a high compression level for fast data transfer at the expense of image quality. Select this option, for example, if you are working in a slow or very busy network.

Note

If images are displayed with reduced image quality as a result of your streaming compression this is indicated by a red bullet in the lower right-hand corner of the window.
Wait until the red bullet has disappeared to assure sufficient image quality for primary diagnosis (see also Low resolution warning).

Protocol configuration

The full scope of protocol configuration options requires a combination of various user level settings. Therefore, even though you may be able to access some of the configuration options described in this section but you may not be able to access all of these options.

- *Prioritizing and disabling protocols*
- *Save Protocol wizard*

Prioritizing and disabling protocols

Use the **File** menu of the **Study Browser** of **View** window (**File > Preferences > Protocols**) or the **View** window **Protocol** menu (**Protocol > Configure Protocols**) to open this dialog box.
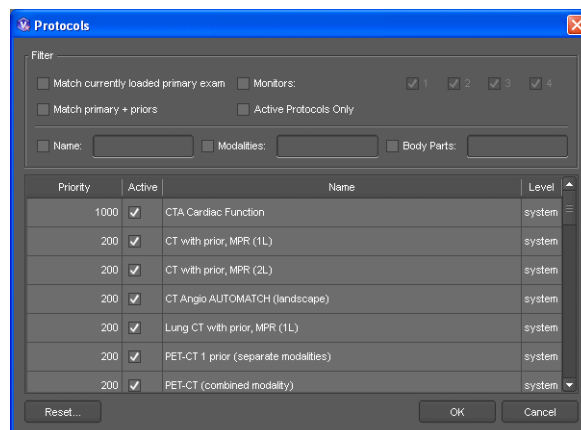
Only protocols with a checkmark in the **Active** columns will be considered when a user loads data and the system selects the protocol best suited for the selected data. Moreover only active protocols are listed in the Protocols menu and presented to users for manual protocol selection.

The **Protocols** dialog box also allows you to prioritize protocols and to enable or disable protocols. Protocols with a high priority ranking are more likely to be selected by the system when a user loads data onto the **View** window. Protocols with a high priority ranking also show up at the top the list when users drop down the **Protocols** menu.

Scroll through the list of all protocols defined for your system in the lower part of the **Protocols** dialog box or use the **Filters** in the upper third of the dialog for a better overview.

Save Protocol wizard

With appropriate user privileges you can modify protocols or create protocols of your own.

Protocol definition workflow

Visage 7 Client expects you to base any protocol definitions on an exisiting protocol. The workflow for protocol modification therefore comprises the following steps:

• Loading appropriate image data onto the **View** window.

• Selecting the protocol you want to modify from the **Protocol** menu.

• Adapting display settings including toolbar and tool card selection.

• Calling up the **Save Protocol** wizard.

• Entering or modifying the protocol name.

Now you can decide to save your modifications right away, or to further review and modify the affected settings. By going through the individual pages of the **Save Protocol** dialog box, you can control the following protocol related settings:

• Defining protocol access and matching criteria.

- Defining toolbar and tool card settings (or accepting interactively made modifications).

- Defining layout and viewer properties (or accepting interactively made modifications).

- Defining image assignment to viewer segments (or accepting interactively made modifications).

- Accepting any global properties you made in the **Preferences** dialog boxes.

  See also *General preferences*.

- Saving your new protocol or protocol modifications.

- Assigning a priority ranking to the new or modified protocol.

  See also *Prioritizing and disabling protocols*.

Save Protocol wizard

Select **File > Save Protocol** to call up the **Save Protocol** wizard.

Note

Because Visage 7 Client expects you to base any protocol definitions on a pre-defined protocol the **Save Protocol** command is dimmed if no image data are currently shown on the **View** window.
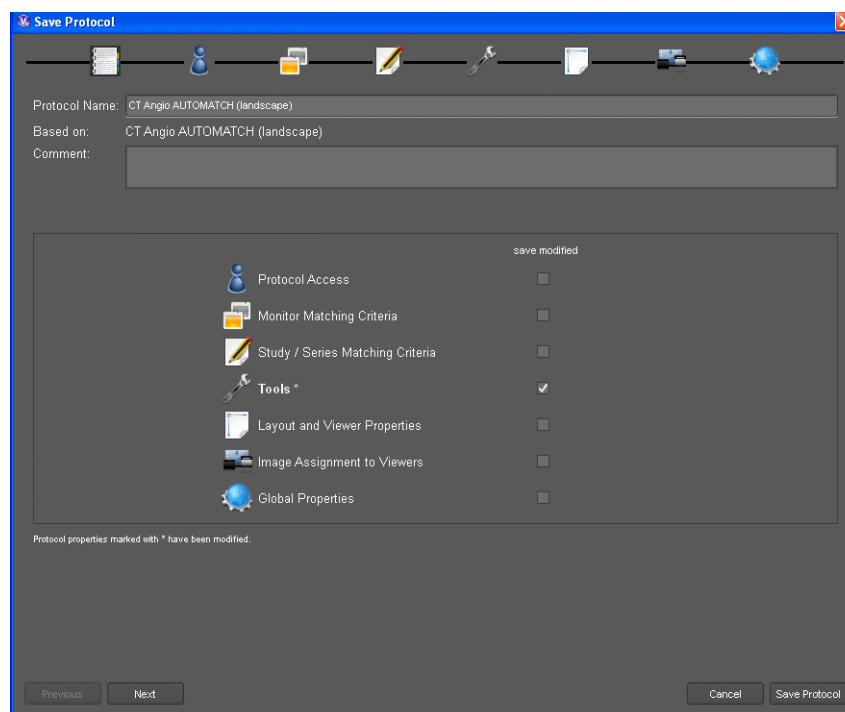
The overview page of the **Save Protocol** wizard indicates which display settings you have already changed interactively on the View window. These categories are shown in bold type and are marked with an asterisk.

Procede through the various pages of the **Save Protocol** wizard and click the **Save Protocol** button when you are done.

Reloading protocols

Each time a user starts a Visage 7 Client session protocols are read into the main memory of the client computer.

If protocols are modified on the server while a client session is still ongoing this client needs to reload protocols in order to be up to date.

Use the **File > Reload Protocol** command to synchronize your protocols with those on the Visage server.

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